

GACCAGCGCTG ACCAGGCGCG GCCAAGCGCG CCCCAGACAC ATGCTGGGCG GGGTACGGCT 2880
 GGGGCAACTG ACCAATAGCG GCGCGGGGTT CCGCGGGGTT AGCAATGGCT TCGGATGCC 2940
 GCGCGGCGCG TACGTAATGC CCGGTGTGCG CCGCGCGCGG TAACCGCGAT CCGCAGCGAA 3000
 TCGGGGGCGT CTATCGCGCG AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Gly Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu

195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu 210 215		220
Ser Gln Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn 225 230	235	240
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val 245 250		255
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala 260 265		270
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met 275 280		285
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu 290 295		300
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser 305 310	315	320
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro 325 330		335
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr 340 345		350
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn 355 360		365
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro 370 375		380
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly 385 390		395

(12) INFORMATION FOR SEQ ID NO:112:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1616 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTTGCGC ACGCAATGCC ACCGGAGTAA ATACCCACAG	60
GCTGATGGCC GCGCGCGGTC CGGCTCCAAAT GCTTGCGCGG GCGCGCGGAT GGCAGACGCT	120
TTCGGCGGCT CTGACGCTTC AGGCGTTCGA GTTGACCGCG CGCGTGAACCT CTCTGGGAGA	180
AGCGTGGACT GGAGGTGGCA GCGACAGGCC GCTTGGCGCT GCAACGCCGA TGCTGATCTG	240

GCTACAAACC GCCTCAACAC AGGCCAAGAC CCGTGGGATG CAGGCGACGG CGCAAGCCCG	300
GGCATACACC CAGGCCATGG CCACGACGCC GTGCGTCCCG GAGATCGCCG CCAACCACAT	350
CACCCAGGCC GTCTTTACGG CCAACCACTT CTTCGGTATC AACACGATCC CGATCGCCTT	400
GACCGAGATG GATTATTCCA TCCGTATGTG GAACCAAGCA GCGCTGGCAA TGGAGGTCTA	450
CCAGGCGGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT	500
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCGGATCTTC GGAATGCGCT CCGCTGGCAG	550
CTCAACACCG GTTGGCCAGT TGGCGCCGCC GCTACGCCAG ACCCTCGGCC AACTGGGTGA	600
GATGAGCCGC CCGATCGACG AGCTGACCCA GCCGCTGCAG CAGGTGACGT CATTGTTGAG	650
CCAGGTGGGG GGCACCGGCG GCGGCAACCC AGCCGACGAG GAAGCCCGCC AGATGGGCGT	700
GCTGGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	750
CGCGGGCGTG CTGCGCGCGG AGTGGCTACC TGGCGCAGGT GAGTCGTTGA CCGCGACGCC	800
GCTGATGTCT CAGCTGATCG AAAAGCGCGT TCGCCCTCTG GTGATGCGCG CCGCTGCTGC	850
CGGATCCTCG CGCAGCGGTG GCGCCGCTCG GGTGGGTGGG GGACCGATGG GCCAGGGTGC	900
GCAATCCCGG GGTCTCCACC GCGCGGCTCT GGTGGCGCGG GCACCGCTCG CCGAGGAGCG	950
TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGCTGAGCTC CGTAATGAC	1000
AACAGACTTC CGGCTCACC GCGCCCGGAG ACTTCCCAAC ATTTTGGCGA GGAAGGTAAA	1050
GAGAGAAAGT AGTCACGAT GGCAGAGATG AAGACCGATG CCGCTACCTT CGCGCAGGAG	1100
GCAGTAATT TCGACCGGAT CTCGGCGCAC CTGAAAACCC AGATCGACCA GGTGAGTTCG	1150
ACCGCAGGTT CTTTCGAGG CCACTGGCGC GCGCGGCGCG GGACGGCTCG CCAGGCGGCG	1200
GTGTTGCGCT TCCAAGAAGC AGCCATAAG CAGAAGCAGG AACTCGACGA GATTCTGAGG	1250
AATATTCTTC AGGCGCGGCT CCAATACTCG AGGCGCGACG AGGAGCAGCA GCAGGCGCTG	1300
TCTTCGCAA TGGGCTTCTG ACTCGCTAAT AGGAAAAGAA ACGGAGCAAA AACTGACAG	1350
AGCAGCAGTG GAATTGCGG GGTATCGAGG CCGCGGCAAG CGCAATTCAG GGAAT	1400

(2) INFORMATION FOR SEQ ID NO:113:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTCTCTGC AGTCTCAGTG CCTCTCTGTG TGACATTTTG 60
 GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAAGGCG TGGCTTGCCA TATCTGTCGG 120
 AGCTTCCATA CCTTCTGTGG GCGGAAGAG CTCTCTGTAG TGGGCCGCCA TGACAACCTC 180
 TCAGATGGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTCGAACCTC 240
 GCGCGATCCC GTGTTTGGCT ATTCTACGCG AACTGGCGCT TGCCCTATGC GAACATCCCA 300
 GTGACGTTGC CTTCGGTCCA AGCCATTGCC TGACCGGCTT CGCTGATGCT CCGCGCCAGG 360
 TTCTGCAGCG CGTTGTTCAG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACGCTGG 420
 TACGCTCTCG AA 480

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met 15
 5
 Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Gly Trp Gln 30
 20
 Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg 45
 15
 Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala 60
 35
 Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr 80
 65
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Tyr 95
 85
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Asn 110
 100
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn 125
 115
 Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp 140
 130
 135

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Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
145                      150                      155                      160

Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
                      165                      170                      175

Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
180                      185                      190

Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
195                      200                      205

Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
210                      215                      220

Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
225                      230                      235                      240

Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
245                      250                      255

Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
260                      265                      270

Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
275                      280                      285

Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
290                      295                      300

Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
305                      310                      315                      320

Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
325                      330                      335

Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
340                      345                      350

Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
355                      360                      365

```

(2) INFORMATION FOR SEQ ID NO:115:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
1                      5                      10                      15

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Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
      20                      25                      30
Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
      35                      40                      45
Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
      50                      55                      60
Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
      65                      70                      75                      80
Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
      85                      90                      95
Gln Met Gly Phe
      100

```

(2) INFORMATION FOR SEQ ID NO:116:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GATCTCCGGC GACCTGAAAA CCGAGATCGA CCGGTGGAG TCGACGGCAG GTTCCTTGCA      60
GGCCCACTGG CCGGGCGCGG CGGGGACGGC CCGCCAGGCC CGGGTGGTGC GCTTCCAAGA      120
AGCAGCCCAT AAGCAGAAGC AGGAAGTCGA TCAGATCTCG ACCAATATTC CTCAGGCGGG      180
CGTCCATATC TCGAGGGCCG ACCAGGAGCA GCAGCAGGCC CTGTCCTCGC AAATGGGGTT      240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAAATTC      300
CGGGGTATCG AGGCGCGGCG AAGCGCAATC CAGGGAAATG TCAGTCCAT TCATTCCTTC      360
CTTGACGAGG GGAAGCAATC CCGACCAAG CTGCGA
                                                                 396

```

(2) INFORMATION FOR SEQ ID NO:117:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
  1           5           10           15

```

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Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30
 Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45
 Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60
 Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCAGTATT TGGCTATTCT AGCGGAAGTC GCGGTGCCCC TATGCGAACA 60
 TCCAGTGCAC GTTGCCTTCC GTCCAAAGCCA TTGCTTGACC GCGTTGCGCG ATCGTCCGCG 120
 CCAGTTTCTG CAGCGCCTTG TTGAGCTCGG TAGCCGTGCG GTCCATTTT TCTGAGACAC 180
 CCTGGTAGCG CTCCGAACCG CTACGCCCG AGGCCGCTGC GAGCTTGCTC AGGGACTGCT 240
 TCCCTGCTTC AAGGAGGGAA TGAATGGACG TGACATTTCG CTGGATTGCG CTTCGCCCGG 300
 CCTGATACCC CCGCAAAATC CACTGCTGCT CTGTCATGTT TTGCTCGGTT TTTCTTTGCT 360
 ATTACCGGCT CAGAAGCCCA TTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCGCAACGCG CCGTGGCAGG GCTCCGTTCC GGGGGCGAGC 60
 TCGCGCCGCG ATCGTTCTTC TGCCCGCAGC CGGCGCTGGA TGAATGAC ACCTGCTACC 120
 TTCCGACGCT TTGCTTGCTT GTCTGTGCGA TAGCGGTGAC CCGCGGCCCG ACCTGGGAG 180
 TGTGAGGGGG CAGGCCCGGT CGTGTGTTCC GCGGGGGAGC CAGACGGTCT GGACGGGAAC 240

GGCGGGGGTTT GCGCGGATGTCG CATCTTTGCC CA

272

(2) INFORMATION FOR SEQ ID NO:120:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:121:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO:122:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10				15		
Glu Gly Arg															

(2) INFORMATION FOR SEQ ID NO:123:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
2 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
2 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala	Pro	Lys	Thr	Tyr	Xaa	Glu	Glu	Leu	Lys	Gly	Thr	Asp	Thr	Gly
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:128:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
1				5					10						15
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn		
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:129:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp	Pro	Pro	Asp	Pro	His	Gln	Xaa	Asp	Met	Thr	Lys	Gly	Tyr	Tyr	Pro
1				5					10						15
Gly	Gly	Arg	Arg	Xaa	Phe										
				20											

(2) INFORMATION FOR SEQ ID NO:130:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp	Pro	Gly	Tyr	Thr	Pro	Gly
1				5		

(2) INFORMATION FOR SEQ ID NO:131:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa	Xaa	Gly	Phe	Thr	Gly	Pro	Gln	Phe	Tyr
1				5					10

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa	Pro	Xaa	Val	Thr	Ala	Tyr	Ala	Gly
1			5					

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa	Xaa	Xaa	Glu	Lys	Pro	Phe	Leu	Arg
1			5					

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa	Asp	Ser	Glu	Lys	Ser	Ala	Thr	Ile	Lys	Val	Thr	Asp	Ala	Ser
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:135:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala	Gly	Asp	Thr	Xaa	Ile	Tyr	Ile	Val	Gly	Asn	Leu	Thr	Ala	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:136:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala	Pro	Glu	Ser	Gly	Ala	Gly	Leu	Gly	Gly	Thr	Val	Gln	Ala	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:137:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa	Tyr	Ile	Ala	Tyr	Xaa	Thr	Thr	Ala	Gly	Ile	Val	Pro	Gly	Lys	Ile				
1				5					10					15					
															Asn	Val	His	Leu	Val
																	20		

(2) INFORMATION FOR SEQ ID NO:138:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(12) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAAGCCTGT CTTGCGCTTT GCGGTGATCG GTTTCGCTC GCTGGGCTG GCGGTGGCG	60
TCAACATCCG ACCGACGCGC GCTTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG	120
GGAAGTTCAT GCGGTGTGTG CCGAGCGAAC AGCAGCGGCC GTTCCGCGCG CTTCCGCCCC	180
ATGATCCCAAC CCGTGGATTC CAGGGCGCGA CCATTCCCGC TGTACAGAAC GTGGTCCCGC	240
GGCCGGGTAC CTCACCCCGG GTGGGTGGGA CGCCGCTTC GCTTGGCGCG GAAGCGCGCG	300
CGGTGCGCGG TTTTGTGCT GCTCCGCTGC CAATCCCGGT CCGATCATC ATTCCCGCGT	360
TCCCGGTTG GCAGCTTGA ATGCCGACCA TCTCCACCGC ACCGCGAGC AGCGCGGTGA	420
CCAGTCCGCG GACGACGCGC CCGACCTACG CGCCGACCA CCGCGTGAGC ACCCGCGCAA	480
CGAGCGCGCG GACGACGCGC GTGACGACG CGCGACGAC GCGCGCGACC ACCCGCGTGA	540
CCAGCGCAGC AAGGACCTGT GGTCCGACGA CGTCCGCGCG GACGACGCTC GCTCCGACCA	600
CGGTGCGCGC GACGACGCTC GCTCCGACGA CGCCACGCG GACGACGCTC GCTCCGACG	660
CGAGCGACGA GCTCCGCGCA CAACCAACCC AACGATGCC AACCCGCGAG CGAGCGGTGG	720
CCCCGCGAC GGTGGCGCGC GCTCCGCGCG CGCGGTCCCG TGGCGCGAAC GCGCGCGCG	780
GGGGCGACTT ATTCCGCGCG TTCTGATCAC GGTCCGCGCT TCACTACGCT CGAGGACAT	840
GCGCGGTGAT GCGGTGACGG TGTGCTGCC CTGTCTCAAC GA	882

(2) INFORMATION FOR SEQ ID NO:139:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(14) MOLECULE TYPE: DNA (genomic)

(15) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACGCTCGCGC CCGCGCGCGC CGCGGATCC GCGTCCGCGC CCACGCGCGC	60
CGGTGCTTCC GGTGCGCGCG TTGCGCGCTT GCGCGCGTC GCGCGCGACC GGTTCGCTGC	120
CTAGGCGGCT GTTACGCGCC TGTTTGCGCG GACGCGCGCC GACACGACG GTACCGCGGA	180
TGGCGCGCTC GCGCGCGCGC GCACCGTTGC CACGTTGCC ACCGTTGCCA CGGTTCGCGA	240
CCAGCGACCC GCGCGCGACCA CCGCGACGCG CGCGCGCGCC CGCACGCGCG GGTTCGCGCT	300
TGTGCGCTGT ACCGCGCGCA CCGCGCTTGC CGCGCTCAC GCGGACGGAA CTACCGCGCG	360
ACGCGGCTTG CCGCGCGCGC CCGCGCGCAC CGGATTGCG ACCGCGCTCA CCGCGCGCTG	420

GGAGTGGCGC GATTAGGGCA CTGACCGGCG CAATCCAGGCG AAGTACTCTC GGTCAACGGAG	480
CAGTTCCAGA CGACACCACA GCACGGGGTT GTGGGCGGAC TGGGTGAAT GCGAGCGTAT	540
AGCGGCTAGC TGTGGCTGC GGTCAACCTC GATCATGATC TCGAGGTGAC CGTGACCGCG	600
CCCCCGAAG GAGGCGCTGA ACTGCGCGTT GAGCGGATCG GCGATCGTT GCGGCACTGC	660
CCAGGCCAAT ACGGGGATAC CGGGTGTGTA AGCGCGCGCG AGCGCAGCTT CGGTTCGCGG	720
ACGTGGTCTC GGGTGGCTTG TTACGCCCTT GTCTTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GCGAGGGGCA TCCACCAACG GTTGCCTCAG CTCT	840

(2) INFORMATION FOR SEQ ID NO:140:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (E) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCGGCG GCGTGAAGTC TCAGATCAGA GAGTCTCGCG ACTCAGCGCG GCGGTTACAG	50
CTTCTCCAG AACAACTGCT GAAGATCTTC GCGCGGAAA CAGGCGGTGA TTGACGCTC	120
TATGACCGGT TGAACGACGA GATCATCCCG CAGATTGATA TGGCAACGCT GGCCTAACAG	180
GTGCGAAGA TGTGTCAAGT GTATGTTTCG GACTCGTGT CCGCGATCAG CTTTGGCGAC	240
GCGCGGTGA TCGTGTGAG CGAGGAAGTC GCGGAGAGCC AGTATCCGAT CGAGACGCTG	300
GACGGATCA CAGTGTTTGG GCGGCGGAG ATGACACGCG CTTTCATCGT TGAGATGCTC	360
AAGGTTGAGC GCGACATCCA GCTTTTCAG ACTGACGCGC ACTACCGAGG CCGGATCTCA	420
ACACCGGAGC TGTCTATAGC GCGCGGCTTC GGTGAGGAG TTAACCGCAC CGAGATCTCT	480
GCGTTCTGCC TGTCTTAAAG CAAGCGGATC GTGTGAGGA AGATCTTAA TCAACAGGCC	540
TTGATTCGCG CACACACGTC GCGGCAAGAC GTTGTGAGA GCATCTCGAC GATGAAGCAC	600
TGCGTGGCTT GGTGTGATCG ATGGGCTCC CTGGCGGACT TGAACGGTT CGAGGAAAT	660
GCGGCAAGG CATACTTCAC CGCGCTGCGG CATCTCTTCC CGCAGGATT CGCATTCGAG	720
GGCGGCTCGA CTGCGCGGCT GTTGAGAGCC TTCAACTCGA TGGTACGCTT CCGGTATTGG	780
CTGCTGTACA AGAATATCAT AGGGGCGATC GAGCGTCAAC GGTGAACGC GTATATCGTT	840

TTCTACACG AGGATTCAAG AGGGCACGCA AGGTCTCGTG CCGAATTCGG CACGAGCTCC	200
GCTGAAACCG CTGGCCGGCT GCTCAATGCC GGTACGTAAZ CCGCTCGGCC CAGGCCGGCC	360
CCCGGGCCGA ATACGACGAG ATCGGACAGC GAATTGCGGC CCAGCCGGTT GGAGCCGTGC	1020
ATACCCCGCG CACACTCACC GGCAGCGAAC AGGCTTGSCA CCGTGGCGGC GCCGTGTGCC	1080
GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTGC GCCCGACTTC CATTGCTTGC	1140
GTTCGGCAGG AG	1152

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCTGCCGA TTGCGCAGGG TGTACTTCCC GGTGGTGTAG GCGGCATGAG TCCCGACGAC	60
CAGCAATCCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACGCGGTCCA CTTGGGCGAT	120
CCGCTCGAGT CCGCCCTGCG CGGCTCTTTC CTGCGGCGAG GTCATCGCAC GTGTTTCCGC	180
CGTGGTTTGC CGCCATTATG CGGCGCGGCC GCGTGGGCGG GCCGTATGCG CGGAAGTTCG	240
ATCAGCACAC CCGAGATAGG GGTCTGTGCA AGCTTTTGA GCGTGGCGCG GCGCAGCTTC	300
GC CGGCAATT CTACTAGCA GAGTCTGGC CGGATACGGA TCTGACCGAA GTGCTGCGG	360
TGCAGCCAC CTTCAATGCG GATGCGGCGG ACGATGGCGC CTGACCGGAT CTTGTGCGGC	420
TTGCGGACCG CGAGCGCGTA GGTGGTCAAG TCCGGTCTAC GCTTGGCGCT TCGCGGACCG	480
TCCCGACGCT GGTCCCGGTT GCGCCGCGAA AGCGGCGGGT CGGTCGCCAT CAGGATGCC	540
TCAGCGCCGC GGCATCTCAC GGCAGTGGC GCGCGGATGT CAGGCATCGG GACATCATGC	600
TCCGTTTCA TCTCTTCGAC CAGTGGGCGG AACAGCTCGA TTCCGKGACC GCCCA	655

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
 1           5           10           15

Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
 20           25           30

Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
 35           40           45

Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala
 50           55           60

Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
 65           70           75           80

Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
 85           90           95

Gln Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
100           105           110

Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
115           120           125

Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
130           135           140

Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
145           150           155           160

Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
165           170           175

Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
180           185           190

Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
195           200           205

Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
210           215           220

Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
225           230           235           240

Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
245           250           255

Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
260           265

```

(2) INFORMATION FOR SEQ ID NO:143:

145

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1           5           10           15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
20           25           30

Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
35           40           45

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
50           55           60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
65           70           75           80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
85           90           95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
100          105          110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
115          120          125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
130          135          140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
145          150          155          160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
165          170

```

(2) INFORMATION FOR SEQ ID NO:144:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

146

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (E) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95
 Gly Gln Leu Arg Arg Gln Phe Tyr
 100

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (E) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGAATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCG GGGCTCGGTT GCGCGGCGCT CATCTTGAAC GA

43

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCTTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCCTGGAA ATCTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCGACGG CTGAGATGAA GACCGATGCC GCT

32

(2) INFORMATION FOR SEQ ID NO:151:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGACGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTC TCCTCCCGGA	60
AGCATGCGGA AACGCCCGA TACGTGCGG GACTGTGGG GGACOTCAAG GACGCCAAGE	120
GCGGAAATG AAGAGCACAG AAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCG GTG TTG ACC GCT GCG CGG CTG CTG CTA GCA GCG GCG GCG	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CTA CCG AGC GGT TCG CTT GAA ACG GCG GCG GCG GCG	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT CTC GCG ACT ACC CCG GCG TCG TCG CCG CTG ACC TTG GCG GAG	316
Gly Thr Val Ala Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT ACC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCG	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG ACG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Glu Gly Thr Gly	
75 80 85	
TCT GGT GCG CGG ATC GCG CAG GCG GCG GCG GCG ACG CTC AAC ATT GCG	460
Ser Gly Ala Gly Ile Ala Glu Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCG TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCG GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Glu Glu Val Asn Tyr Asn	
120 125 130 135	
CTG GCG GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCG ATG TAC CAG GCG ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Glu Gly Thr Ile Lys Thr Trp Asp Asp Pro Glu Ile Ala	
155 160 165	
GCG CTC AAC CCG GCG GTG AAC CTG CCG GCG ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	

170	175	180	
CAC GGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG			746
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu			
185	190	195	
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC			756
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr			
200	205	210	215
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC			844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn			
220	225	230	
GGC GGC ATG GTG ACC GGT TGC GCG GAG ACA CCG GGC TGC GTG GGC TAT			892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr			
235	240	245	
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CCG GGA CTC GGC GAG			946
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Gln			
250	255	260	
GCC CAA CTA GGC AAT ACC TCT GCG AAT TTC TTG TTG CCC GAC GCG CAA			988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln			
265	270	275	
AGC ATT CAG GCC GCG GCG GGT GGC TTC GCA TCG AAG ACC CCG GCG AAC			1036
Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn			
280	285	290	295
CAG GCG ATT TCG ATG ATC GAC GCG CCC GGC CCG GAC GGC TAC CCG ATC			1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile			
300	305	310	
ATC AAC TAC GAG TAC GCC ATC CTC AAC AAC CCG CAA AAG GAC GGC GGC			1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala			
315	320	325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC			1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly			
330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG AGC ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCTCTGTT GACCACGACG CGACAGCAAC CTCGCTCGGG CCATCGGGCT GCTTTGCGGA			1313
GCATGCTGCC CGGTGCGGAT GAAGTGGGCC GCGTGGCCCG GGCATCCGGT TGCTTGCGTG			1393
GGATAGGTGC GGTGATCCCG CTCCTTGGCC TGCTCTGGGT GCTGTTGGTG CTGGTCATCG			1453

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AGGCGATGGG TGGGATCAGG CTCACCGGGT TGCATTTCTT CACCGCCACC GAATGGAATC 1513
CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGGGTC GCGCATCCGG TGGGGGCTTA 1573
CTACGGGGGG TTGCGCTGA TCGTGGGAC GCTGGGACC TCGGCAATCG CCTGATCAT 1633
CGCGTCCCG GTCTGTGTAG GAGCGCGCT GGTGATCGTG GAACGCTGC CGAAACGGGT 1693
GGCGGAGGCT GTGGGAATAG TCTTGGATT GCTGCGCGA ATCCCGAGCG TGGTCGTGG 1753
TTTGTGGGG GCAATGACCT TCGGGCCGTT CATGCTCAT CACATCGCTC CGGTGATCGC 1813
TCACAACGCT CCCGATGTGC CGTGCTGAA CTACTGCGC GCGACCCCG GCAACGGGGA 1873
GGGCATGTTG GTGTCGGCTC TGGTGTGGC GTTGATGTC GTTCCGATTA TCGCACCCAC 1933
CACTCANGAC GTGTTCCGCG AGGTGCGGTT GTTCCCGCG GAGGGCGCGA TCGGGAATTC 1993

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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1           5           10           15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20           25           30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35           40           45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50           55           60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65           70           75           80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85           90           95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100          105          110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115          120          125
Ala Gln Gln Val Asp Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys

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110	135	140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr 145 150 155 160		
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro 165 170 175		
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr 180 185 190		
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly Trp Gly 195 200 205		
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly 210 215 220		
Ala Leu Gly Gln Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu 225 230 235 240		
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala 245 250 255		
Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Ser Gly Asn 260 265 270		
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe 275 280 285		
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro 290 295 300		
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Gln Tyr Ala Ile Val Asn 305 310 315 320		
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu 325 330 335		
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val 340 345 350		
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu 355 360 365		
Ile Ala Thr Ile Ser Ser 370		

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1993 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCACACCGA ACAGCTGTTC TCCTGCGCGA	60
AGCATGCGGA AACCGCCCGA TACGTGCGCG GACTGTGCGG CGAGCTGAAG GACGCCAAGC	120
GCGGAATTG AAGAGCACAG AAGGGTATGG CTGAAAAATT CGTTTGCGTA CGCTGTGCGC	180
CGTGTGACG GTCGCGCGCG TCTGCTAGC AGCGGCGGGC TGTGCTGGA AACCAACGAG	240
CGTTTGGCT GAACGGGGG CGGCGCGCG TACTGTGCG ACTACCCCG CGTGTGCGC	300
GTTGACGTTG GCGGAGACCG GTAGCAGGCT GCTCTACCG CTGTTCAACC TGTGGGTCC	360
GGCTTTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGCTGC	420
CGGATGCGCG CAGCGCGCG CGGGGACGCT CAACATTGG GCTTCGAGG CCTATCTGTC	480
GGAACTGTAT ATGCGCGCG ACAAGGGGCT GATGAACAT CGCTAGGCA TCTCGGTCGA	540
GCAGCTCAAC TACAACCTGC CGGAGTGAAG CGAGCACCTC AAGCTGAAG GAAAGTCTT	600
GGGGGACATG TACCAGGCGA CCATCAAAAC CTGGGACGAC CGCGGATCG CTGCGCTCAA	660
CCCCGGGTG AACCTGCGCG GCACCGCGGT AGTTCGCGTG CAGCGCTCCG ACGGGTCCCG	720
TCACACCTTC TTCTTACCG AGTACCTGTC CAAGCAAGAT GCGGAGGCT GGGGCAAGTC	780
GCCCCGCTTC GGCACACCG TCGACTTCCC GCGGTGCGG GGTGCGCTGG GTGAGAACGG	840
CAAGCGCGCG ATGGTGACCG GTTGCGCGCA GACACCGGCG TCGTGCGCT ATATCGGCAT	900
CAGCTTCTC GACCAAGCGA GTCAACGGGG ACTCGCGGAG GCCCAACTAG GCAATAGCTC	960
TGGCAATTTC TTCTTCCCG ACGCGCAAG CATTCGGCT GCGGCGCGTG GCTTGCATC	1020
GAAACCCCG GCGAACCAGG CGATTTCGAT GATCGACGG CCGGCGCGCG AGGGCTACCC	1080
GATCATCAAC TACGAGTAC CCATGCTCA CACCGGCAA AAGGACGCG CCACCGGCGA	1140
GACCTTCGAG GCATTCTTGC ACTGGGCGAT CACCGACGCG AACAGGCGCT GCTTCTGCGA	1200
CCAGGTTGAT TTCCAGCGCG TCGCGCGCG GGTGGTGAAG TTGTCTGAG CGTTGATCGC	1260
GAGGATTTC AGCTAGCTTC GTTACCGAG ACGCGACAG AACCTCGGTC GGGCGATCGG	1320
GCTGCTTTGC GGAGCATGCT GCGCGCTGCG GTTGAAGTCT GCGCGCGTGG CCGCGGATCG	1380
CGGTGTTGG GTGGGATAGG TCGGGTATC CCGCTGCTTG CGCTGCTCTT GGTGCTGCTG	1440
GTGCTGCTCA TCGAGGCGAT GGTGCGGAT AGGCTCAAG GGTTCGATTT GTTACCGCGC	1500
ACCGAATGGA ATCGAGGCAA CACCTACGCG GAACCGTTG TCACCGAGCG GTGCGCGATC	1560
CGGTGCGCG CTACTACGCG CGCTTGCCTG TGATGCTCG GACGCTGCG ACCTCGGCAA	1620

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TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
TCCCGAAACG GTTGGCCNAG GCTGTGGGAA TAGTCTGGA ATTGCTCGCC GGAATCCCCA 1740
GGCTGCTGCT CAGTTTGTGG GGGGCATGA CATTGGGAC GTTCATCGCT CATCATATCG 1800
CTCCGGTGAAT CGGTGACAAC GCTCCCGATG TCCCGGTGCT GAACACTTG CCGCGCGACC 1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTG GCGGTGATG GTCGTTCCCA 1920
TTATCGCCAC CACCACTCAT GACCTGTTCG GGCAGGTGCC GGTGTTGCCC CGGAGGGCG 1980
CGATCGGAA TTC 1993

```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1           5           10           15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20           25           30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35           40           45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50           55           60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65           70           75           80
Ile Thr Ala Glu Gly Thr Gly Ser Gly Ala Gly Ile Ala Glu Ala Ala
85           90           95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100          105          110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115          120          125
Ala Glu Glu Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130          135          140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Glu Gly Thr Ile Lys Thr
145          150          155          160

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155

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 163 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(x) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCTTGACC ACCACTGGG TGTGGAATC GGTGCCCGGA TTGAAGTCCA GGTACTCCTG 60
 GGTGGGCGCG CCGAACAAT AGCGACAAGC ATGCCAGCAG CCGCGGTAGC GTTGACGGT 120

GTAGCGAAAC	GGCAACGCGG	CGCGTTGGG	CACCTTGTTC	AGCGCTGATT	TGCACACAC	186
CTCGTGGAAG	GTGATGCCGT	CGAATTGTGG	CGCGGGAAGG	CTGCGGACCA	GGCGGATCGG	240
CTGCAACCCG	GCAGCGCCCG	TGTCACCGG	GGATCCCGTT	CACCGCGACC	GCTTGCCTGG	300
CCCAACGCAT	ACCAATTATC	GAACAACCGT	TCTATACCTT	GTCAACGCTG	CGCGCTACCG	360
AGCGCGGAC	AGGATGTGAT	ATGCCATCTC	TGCGCGCACA	GACAGGAGCC	AGCGCTTATG	420
ACAGCATTCG	GCGTCGAGCC	CTACGGGCGG	CGGAAGTACC	TAGAAATCGC	CGGGAAGCCG	480
ATGCGGTATA	TGGACGAAGG	CAAGGGTGAC	GCCATGGTCT	TTCAGCACCG	CAACCCGACG	540
TGCTCTTACT	TGTGGCGCAA	CATCATGCCG	CACCTGGGAG	GGCTGGGCGG	GCTGTGCGCC	600
TGCGATCTGA	TGGGATGCGG	CGCGTCGGAC	AAGCTCAGCC	CATCGGAGCC	CGACCGTAT	660
AGCTATGGGG	AGCAACGAGA	CTTTTTGTTC	GCGCTGTGGG	ATGCGCTCGA	GCTCGCGGAC	720
CACGTGTGAC	TGTTGCTGCA	CGACTGGGCG	TGCGCGCTCG	GCTTCGACTG	GGCTACCCAG	780
CATCGCGACC	GAGTGCAGGG	GATCGCGTTC	ATGGAAGCGA	TGTCACCCCG	GATGAGCTGG	840
GGCGACTGGC	CGCGCGCGGT	CGCGGGGTGG	TTCAGGGGTT	TCCGATCGCC	TGAGGGGAGG	900
CCAAATGCGT	TGGAGCACA	CATCTTTGTC	GAACGGGTGC	TGCGCGGGCG	GATCGTGCGA	960
CAGCTCAGCG	ACGAGGAAAT	GAACCACTAT	CGCGCGCCAT	TGCTGAACCG	CGCGCAAGAC	1020
GCTCGCGCCA	CGTTGTCTGT	GCCACGAAC	CTTCCAATCG	ACGCTGAGCC	CGCGGAGGTC	1080
GTGCGGTTCG	TCAACGASTA	CGCGAGCTGG	CTCGAGGAAA	CGGACATGCC	GAATCTGTTC	1140
ATCAACGCGG	AGCGCGCGCG	GATCATTCAG	GGCGSCATCG	GCTACTATGT	CAGGAGCTGG	1200
CCCAACCGAG	CGGAATATCA	AGTGGCGGCG	GTGCAATTCG	TTCAGGAGGA	CAGCGATGGC	1260
GTGCTATGCT	GGCGGGGGCG	TGGCGAGCAT	CGCGGACCTG	GGAGCGCTCT	CATTTCACGA	1320
GACCAAGGAT	GTGATTTCCG	GCGAAGGCGG	CGCGCTGCTT	GTCAACTCAT	AAGACTTCTT	1380
GCTCGGGGCA	GAGATTCTCA	GGGAAAAAGG	CACCAATCGC	AGCGGCTTCC	TTCGCAACGA	1440
GGTCACAGAA	TATAGTGGCG	AGGACAAAGG	TCTTCCTATT	TGCGGAGCGA	ATTAGTCTCT	1500
GCCTTTCTPAT	GGGCTCAGTT	CGAGGAAGCC	GAGCGGATCA	CGCGTATCGG	ATTGAGCTTA	1560
TGGAACCGGT	ATCATGAAGG	CTTCGATCA	TTGGAAGAGC	GGGGGCTCTT	GCGCGCTCGG	1620
ATCATCGGAC	AGGGCTGCTC	TCACAACCGC	CACATCTACT	AGTGTCTACT	AGCGCCGAGC	1680
GGCGATCGGG	AGGAGGTGCT	GGCGGCTCTG	ACGAGCGAAG	GTATAGGCGC	GCTCTTTCTAT	1740

TAAGTGCCTC TTCACGATTC GCGGCGCGGG CGTCGCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACAGGTC TCCTTAGGCG CTCCTTCCCG TGAATGCCCA TATCACGCAC	60
GGCATGTTTC TGGCTGTGGA CTTTCGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CCGGGGACG GTTCGCGGAA GCGGCGCAGG ATGTGCTGGA GCGCGCGCCG	180
CGCGTCCGCC CAGCGGACCG CTGGATGCTC AGCCCCGGTG CCGGACCTTA GCCAGCGTTT	240
GGCGGTGTC GTCCACAGTG GTACTCGGT GAGGAGCGCG CCGCGTGCCT GGGTGAAGAC	300
CCTGACCGAC GCGCGCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CAGCTTCCGC TGGCAGGGA CTTGTACGAC CTGAACCACT TCGCTTCGCG	60
AACGATTGAC GAACCGCTCG TCGGCGGCT CTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GCGCACTACG GTTCGAAGAC GTCTTCGCGC CCGCGAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCGCT CTTGTGCTA TGGCTGCGTG	240
GGAAGCTCCG GTTCGGAAGC GATTTCGCTT CTTGACTGAC CTCGACGCGC ACGAGCAGCG	300
GTGGGCGGCG TCGGACGAAC GGCACGCGCG CGAAGTGGAG AACGCGCTGG CCGTCTGCGG	360
GTCTGTATCA ACCTGCCGCG GATCGTCCCG TTCCGTGCGC ACGGTGCGCG CTGGACCGCG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CTAATCGCGC TGTGTGCTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCG TGATTCAGCA GACCAATGG	540
AACGCGCGCG GCGAAACCT CTCGAGAGTG ATCGCGCTCC CCGCGGAACC CTGCGGTGCT	600
GGGTTCATTC GGACATCGGT CCGCTCGCG GATCTGCGT GACGCGCGCG CTGAAGGAGT	660

GGAGCGCGGC	GCTGCACGC	CTGCTGGACG	GCCGGCAGAC	GGTGTCTGCTG	CGTAAGGCGG	720
GGATCGGCGA	GAAGCGCTTC	GAGGTGGCGG	CCCACGAGTT	CTTGTGTGTC	CCGACGGTCC	780
CGCACAGCCA	CGCGGAGCGG	GTTCGCGCGG	AGCACCGCGA	CTTGTCTGGC	CCGCGGCGCG	840
CCGACAGCAC	CGACGAGGT	GTGCTACTCG	GGGCGGCAGC	GAAAGTTGTT	GCCGCACTGC	900
CGGTTAACCG	GCCAGAGGGT	CTGGACGCCA	TGAGGATCT	GCACATCTGG	ACCGCCGAGT	960
CGGTGCGCGC	CGACCGGCTC	GACTTTGCGC	CCAAGCACAA	ACTGGCGGTC	TTGGTGGTCT	1020
CGCGGATCC	GCTGGCGGAG	CCGCTCGGCG	TGGCGGATAG	GCGCGAGTAC	GGCGTTTCCA	1080
CCAGCTGGGT	GCAGCTGCGC	GTGACGCGGA	CGTTGGCGGC	GCGCGTCCAC	GACGAGGCGG	1140
CGGTGGCGGA	GGTGGCGGCG	CGGCTCGCGG	AGCGCGTGGG	TTGACTGGGC	GGCATGGCTT	1200
GGGTCTGAGC	TGTACGCGCA	GTGCGCGCTG	CGAGTGATCT	GCTGTGGGTT	CGGTCCGTGC	1260
TGGCTGCAAT	TGACGCGCGG	GGCAACAGCA	GCATTGGCGG	CGCCATCCTC	CGCGCGCGCG	1320
GGCGCCACCG	CTACAACC					1328

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGCGCGCAC	CGCGGCGACC	GGCGGTACCG	GCGGCAACGG	GGGTGACGCC	GCTGTGTGG	60
TGGCTTGGG	CGCGAAGGCG	GACCTGGCT	TGCTGGCGG	CAAGGCGGT	AACGGCGGAA	120
TAGGTGGGG	CGCGGTGACA	GCGCGGGTGG	CGGCGGACGG	CGGCACCGCG	GGCAAGGTG	180
GCACCGCGCG	TGCGCGCGCG	GCGGCAACG	ACGCGGGGCG	CACCGCAAT	CCCGCGGTA	240
AGGCGGCGCA	CGCGCGGATC	GCGGGTGGCG	CGGGGCGCGG	CGGCGCGGCT	GGCACCGGCA	300
ACGCGGCGCA	TGCGGCGAAC	C				321

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GAAGACCCCG CCGCGCCATA TCGATCGGCT CGCGACTAC TTTCGCCGAA CGTGCACGGC      60
GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CGGCACCGGA TGGCTGCTGC      120
CGTTCGGCTC CGAATCTCTC ACTTCGGGCG AAGCGCGACG GCACCGCGGA ATCACCAGGG      180
CGGTCCACGA TTCGGGTGCA AAGATCTCTC TGCAAATCTT GCACGCGCGA CGCTAGGCTT      240
ACCACCGACT TCGGTCACAG GCTTCGCGGA TCAAGGGGCT GATCAGCGCG TTTCGTGCGC      300
GAGCACTATC GGCTCGCGGG GTGGAAGCGA CCGTCGCGGA TTTCGCGGCG TGGCGCGACT      360
TGGCGCGCGA TGGCGGCTAC GACGCGGTCC AATCATGCG CAGCGAAGGG TATCTCTCTCA      420
ATCAGTTCTT GCGCGCGCGG ACCACACAGC GCACCGACTC GTGGCGCGCG ACACGCGCGA      480
ACCGTGGCGG GT

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(2) INFORMATION FOR SEQ ID NO:161:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(21) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala      1
1      3      10      15
Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg      20
20      25      30
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr      35
35      40      45
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro      50
50      55      60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu      65
65      70      75      80
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys      85
85      90      95
Tyr Leu Gln Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys      100
100      105      110
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu      115
115      120      125
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala

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130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly 145	150	155 160
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu 165	170	175
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp 180	185	190
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg 195	200	205
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp 210	215	220
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser 225	230	235 240
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg 245	250	255
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn 260	265	270
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr 275	280	285
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val 290	295	300
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met 305	310	315 320
Pro Lys Leu Phe Ile Asn Ala Gln Pro Gly Ala Ile Ile Thr Gly Arg 325	330	335
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val 340	345	350
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp 355	360	365
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg 370	375	380
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Pro Ala Cys Gln Leu 385	390	395 400
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln 405	410	415
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly 420	425	430

Glu Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Glu Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Glu Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Glu Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45
 Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Glu Phe Arg His Val
 50 55 60
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Glu Arg Asp Asp Leu
 65 70 75 80
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Glu Arg Gly
 85 90 95
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110
 Phe Leu Val Ala Glu Leu Ser Glu Asp Arg Pro Gly Glu His Pro Phe
 115 120 125

Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:163:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT GGTGGTGGT GGTGGCAAG GCGTTTGGGC GATTGGCCGG CTACTGCTCC 50
 GCGATGCAAG CGATGCGCGG TTCTGCGGAT GCGTTGCGCC AAGAGCTGCG GGTAGCGGA 100
 ATGCGGCTGT CGGTGATCA CCGCGGGCTG ACCGAGACAC GCGTTTGGC CACCTGCGAC 150
 CCGCGCGACA TCGCGCGCGC GTTTCGCGAC CTCACGCCCA TTGCGGTTCA CTGGGTGCGG 200
 GCAGCGGTGC TTGACGGTGT GGCG 264

(2) INFORMATION FOR SEQ ID NO:164:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1171 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTGGCGGA CGATGACSTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG GCGGACCACG	60
AAGCGCGTGC GATCTTACC CGGGAAGCAG TGCGTGAGCA CCGGGCGTCC GCGGGCAAGC	120
AGTGTGACGA CACGATGTAG GCGCGCGTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TGCTCGGTCA TGTAGCGGGT GCGCGCGTCA TTATCGACT GCGTGGATTG GCCGACTCG	240
CGTTGGAGC CGTCATTGCT TAGCAGCCTC TTGAATCGCG TTTCGTCCGG CCGTGAGTCG	300
TGGCGTCTAT CATCGGCGAG CTCGGGGAAC GGCAGCAGGT GGCCTCGAT GCGTCCGGA	360
ACCGTCTCTG GACCGCGCGG GCGAACCTTC CCGGACGACC GCAGGTCCGC AACGTCCGTG	420
ATCGCCAGCC GCGCGACGCT TGCCCTCGT GCGGAATTCC GCAAGAGGCT GCGGAGCCAC	480
GCGGCATCAC CAAGCAACGC TTGCTTCAGTA CGGATCGTCA CTTCGCGATC CCGGAGACCA	540
ATCTCTCTCG GCGGCATCGT CAGATCGCGC TCGTGGCTTG ACAAGAACGG CCGCAGATGT	600
GCGAGCGGCT ATCGGAGATT GAACCGCGCA GCGAGTTCTT CAATCGCTCG GCGCTCGCGC	660
ACTATTGCGA CTTTCGCGCG CTCGCGGTAT TCAGCAGCA TCGGAGTCTC GACGAACTCG	720
GCGCACTTAA CCGACGCGGT AGCTCCCGCG CTGACGCGGA GGCATCGCGG GTGATCTTTG	780
GCGCTAGGCT CGTAGCGCTT GATCCACCGC TTTCGCGTGC CCGCGCGGAG GCGGATCAGC	840
TTATCGACTT CCGCGTATCG CAGCGGCAAG CTGGGCGCGT TCGTCAAGGT CAAGAACTCC	900
ACCATCGCGA CCGGCACCAA GGTGCGCGAC CTGACCTACG TCGGCGACGC CGACATCGGC	960
GAGTACAGCA ACATCGCGCG CTCGAGCGTG TTGCTCAACT ACGACGGTAC GTCCAAACGG	1020
GCGACCAACG TCGTTTCGCA CGTACGGACC GGTCCGACA CGATGTTCTT GCGCCAGATA	1080
ACCATCGCGC ACGGCGCGTA TACCGGGGCC GGCACAGTGG TCGGGGAGGA TGTCCCGCGC	1140
GCGCGCGTGG CAGTGTCCGC GCGTCCGCAA C	1171

(2) INFORMATION FOR SEQ ID NO:165:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCAAGGCGG CACGGCGGG GCGGCATGA ACAGCTCGA CCGCTGCTA GCGGCCAAG	60
ACGGCGGCCA AGGCGGCACC GCGGCGACCG GCGGCAACGC CGGCGCGCGC GGCACGAGT	120
TCACCCAAGG CGCGACGGC AACCGCGCA ACGGCGGTGA CGCGCGGTC GCGGCAACG	180
GCGGAACGG CGGAACGGC GCAGACAACA CCACACCGC CGCGCGC	227

(2) INFORMATION FOR SEQ ID NO:166:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CGTGGCCAC ATGGCGGGC AGGCGGTAG CGTGGCGCC GGTCTACCC CAGGCCCAA	60
GCGCGCCAC GCTTCACTC CACCCAGCG CGCGACGCG GCGACGCGC GCAACGCGC	120
CAACTCCAA GTGCTGGCG GCAACGCGC CGACGCGCG AATGGCGCA ACCGCGGCG	180
CGCGCGGCG GCGCGGCGC GCGCGCGCG CGCGACGCG GCTTTGGTG GCATGAAGTC	240
CAACGCGAC AACCTGGTG AAAACGGCG AAACGTAAC CCGCGCGCA ACCTGGCGC	300
CGGC	304

(2) INFORMATION FOR SEQ ID NO:167:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGAGCTT GCGAGGCTG TATAACAAG ACAACATGA CCAGCGCGG CTGGGTAGC	60
TGATGAGCT ATTAAACAGT GCGGCTTCA GCGGCGAGG CGAGCACCGC GCGCGGATC	120
TGATGGGTGA GGTCTACGAA TACTTCTTG GCAATTCTG TCGCGCGAA GCGAAGCGG	180
GTGGGAGTT GTTACCGG CCGAGGCTG TCAGGTGAT CGTGGAGTG CTGGAGCGT	240
CGAGTGGGG GTGTATGAC CGTGCTGCG GTTCGAGG CATGTTTGG CAGACCGAG	300
AGTTGATCTA CGAACACAG GCGATCCGA AGGATGTCT GATCTATGC CAGGAAAGCA	360
TTGAGGAGAC CTGGCGGATG GCGAAGATGA AACTGCGCAT CCAGGCGATC GACAACAAGG	420

GGCTGGGGC	CCGATGGAGT	GATACCTTCG	CCCGCGACCA	GCACCGGAC	GTGCAGATGG	480
ACTAGTGTAT	GGCCAATCCG	CGTTTCAACA	TCAAAGACTG	GGCCCGCAAC	GAGGAAGACC	540
CACGCTGGCG	CTTCGTGTTT	CGCCCGGCCA	ATAACGCCAA	CTACGCATGG	ATTGAGCACA	600
TCTGTACAA	CTTGGCGCGC	GGAGTCCGGG	CGGGCTGGT	GATGGCCAAAC	GGTGGATGT	660
CGTCGAATC	CAACGGCAAG	GGGATATTC	GCAGCCTAAT	CGTGGAGGGG	GATTGGTTTT	720
CGTGCATGCT	CGGTTACCC	ACCCAGCTGT	TCGCGAGCAC	CGGAATCCGG	GTGTGCTGT	780
GGTTTTTTCG	CAAAACAAG	CCGGCAGGTA	AGCAAGGGTC	TATCAACCGG	TGCGGCGAGG	840
TGCTGTTCAT	CGAGCTCGT	GAACGGGGG	ACCTAGTGGG	CGGGGCCGAG	CGGGCGCTGA	900
CCAACGAGGA	GATCGTCGCG	ATCGGGGATA	CGTTCCACCG	GAGCAGCACC	ACCGGCAACG	960
CGGGCTCCGG	TGTTGCGCGG	GGTAATGGGG	GCATCGGCTT	CAACCGGCGG	GGCGGTGCTG	1020
CGCGGGCGCG	CGGCAACCGG	GGTGTGCGCG	GGGTTCCTTT	CGGCAACGCT	GTGGCGGGCG	1080
ACGGCGGCAA	CGGCGCAAC	GGCGGCCAGG	GGGGCGACGG	CACGACGGCG	GGCGCGGGCG	1140
GCAGGGCGCG	CAACGCGCAG	AGCGGTGCGG	CCAGCGGCTC	AGGCTGTGTC	AAGGTCACCG	1200
CGGGCCACGG	CGGCAACGGC	GGCAATGGCG	GCAACGGCGG	CAACGGCTCT	CGGGCGGGCG	1260
GGGGCCAGGG	CGTGTGCGCG	GGCAGCGCGG	GCAACGGCGG	CCAGCGGGCG	GGTGGCCACCG	1320
GGGGCGCGAG	CGGCAAGGGC	GGCAACGGCA	CGAGCGGTGC	CGCCAGCGCG	TAGGCGCTCA	1380
TCAACGTCAC	CGCGCGGCAC	GGCGGCAACG	GGGGCAATGG	CGGCAACGGC	GGCAACGGCG	1439

(1) INFORMATION FOR SEQ ID NO:168:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(1) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGCGCGGGCG	GGCGGATTTT	TCTGTGCTT	TGATTGTGCG	TGGGGATAAC	GGCGGTGATG	60
GTGTAAACGG	CGGGATGGCG	GGGGCTGGCG	GGGCTGGCG	CCCCGGGGCG	GGCGCGGGCG	120
TGATCAGCTT	GCTGGGCGCG	CAAAGCGCGG	GGGGGGGGCG	CGGAGCGCGC	GGGGCGGGCG	180
GTGTGGGGCG	TGAGGGCGGG	GCCGGCGGGC	CCGGCAACCA	GGCTTCAAC	CGAGGTGGCG	240
GGGGGGGGCG	CGGCTGATC	AGCTGTCTGG	GGGGCCAAGG	GGCGGGGGCG	GGGGCGGGCA	300
CGCGGGGGCG	GGCGGTGTTT	GGCGGTGAC				329

(2) INFORMATION FOR SEQ ID NO:169:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGG ACCAGACAGA CGGTGGGGAT GGGCGGAGGT AACTGTGGTG 60
 CGCGCGGGCT GATCGGCAAC 80

(2) INFORMATION FOR SEQ ID NO:170:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCAGAC CGCGGCAATC GCGGAGCTTC GCGGCCCAAT ATCCAGCTCA 60
 AGGCGTACTA CTTACCGTGG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA 120
 TCAAGGTGAT CGACCGCGAC GGGCATCGAG GCGGTCTGCG GCGGCTCGG GCAGGATCGG 180
 CCGCGGCGCA CTTGCGCGCG CAAGCGGCT CATCGCTCG AACGCGGCG ATCCTGTGAG 240
 CACACTGAT GCGCGCAAC GAGATTCGT CATTGTCAA GCGGTGTTC ACCGAGGGA 300
 CGGTATTAC GTAIGTCAC CTATGTCAC TCGAAGAACC GGCATAACGA TCCCGTATC 360
 GCGGACAGC CCAGGAGTC AGACCGTTA CA 392

(2) INFORMATION FOR SEQ ID NO:171:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CGGCGGCGAC CGGTTTGGC GGTGGGCGG GCGGGGCGGG CGGGCAGGGC 60
 GGTATCAGCG GTGCGCGGG CACCAACGGC TGTGGTGCG CTGGCGGCAC CGGCGACAA 120
 GCGGCGCGCG GGGCGGCTGG CGGGCGCGG GCGGATAACC CCACCGCAT CGGCGGCGCC 180

GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCGGGCG GGGCGGTGG CCGCATCGGT	240
ACCGGCGGCA CCGGCGGGCG GGTGGGAGC GTCGGTAAAG CCGGGATCGG CGGTACCGGC	300
GGTACGGGTG GTGTGGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCGCG TGGCAGCAGC	360
GCTACGGGTG GCGCGGGGTG CGCGGGCGGC GCGGCGGAG AAGGCGGACC GGGCGGCAAC	420
AGCGGTGTGG GCGGCACCAA CGGCTCGGCG GCGCGCGGCG GTGCAAGCGG CAAGGCGGCG	480
ACCGGAGGTG CCGGCGGGTG CCGGCGGAG AACCGCACCG GTGCTGGTGT CCGCG	538

(2) INFORMATION FOR SEQ ID NO:172:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGAGCTGCG CCGGGCGATA CCGGGGTAC CCGACTACTAC ATCATCGGCA CCGAGAAATCG	60
GCGGCTGCTG CAACCGCTGC GCGCGGTGCC GGTCAATCGGA GATCGGCTGG CCGACCTGAT	120
CCAGCGGAAC CTGAAGGTGA TCGTCAACCT GCGCTACGGC GACCGGAAGT ACGGCTACTC	180
GACGAGCTAC GCGGATGTGC GAACGCGGTT CCGGCTGTGG CCGAAGCTGC CGGCTCAGGT	240
CATCGCGCAT GCGCTGGGCG CCGGAACACA AGAAGGCATC CTGACTTCA CCGCCAGCT	300
GCAGGCGCTG TCGGCGCAAC CGCTCAGCT CCGCAGATC CAGCTGCGCG AACCGCGGA	360
TCTGGTGGCC GCGGTGGGCG CCGGACCGAC GCGGCGGAG GTGGTGAACA CGCTCGCCAG	420
GATCATCTCA ACCAATACG CGCTCTGCT GCCCAGCGTG GACATCGGCC TCGGCTGCTC	480
ACCGAGCTGC CGCTGTACAC CAGCGAAGTG TTGCTCAGGC AACTCGCTGC GGGCAATCTG	540
ATCAACGCGA TCGGCTATCC CCGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG	600
CGGCGTGAA TTGCTACCC TCGTGGGCG GCGCTCGGAC ACCGTTGAA ACATCGAGGG	660
CGCTGTCAAC TACCGATTC CCGACGGCAT	690

(2) INFORMATION FOR SEQ ID NO:173:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ACGGTGACGG CGGTACTAGC GCGGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT	60
TGGGACACAG CGGGGTGGC GGCACCGGTG GCGCGGCGAG CACCGGTACT GCAGTGGCG	120
GCTCTGGGGG CACCGCGCGC GACGGCGGGA CCGGCGGGCG TGGCGGCTTG TTAATGGGCG	180
CGCGCGCGCG CGGGCACGGT GGCACGTGGC GCGCGGGCGG TGCCGTGTCT GACGTTGGCG	240
GCGCGGGCGG GGGCGGCGGG GCGGGCGGGA ACGGCGGCGC CGGGGGTCAA GCGGCCCTGC	300
TGTTGGGGCG CGCGCGCACC GCGGGAGCGG GCGGCTACCG CGGCGATGCC GGTGGCGGCG	360
GTGACGGCTT CGACGGCAGG ATGGCCGGCC TGGTGGTAC CGGTGGC	407

(2) INFORMATION FOR SEQ ID NO:174:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTGAG CGCATCCGCC TCGGGGCGAA GCGATTCCGC GGTCTCAGCG AAGAACATCG	60
TGCACGCGCG GCGCGGACCC AGCCCGGTGC GCTGCGCGGC GTCGAACGCC TCACGACGGC	120
ACAGCCAGTC CTGCGCGGCC TCGAGGGCGA ACACGTGGGT GTCACCGGTG TAGATCGCGG	180
GGATGCGCGC CTCGCGCAAC GCATTCCGGC AGCGCGCGCG GTCTTTGTGA TGCTGACGGA	240
TCACGGCGAT GTTTCGCGCC ACCACGCGCC GCGCGGCGAA GGTGGCGCGG CTGGCCAGTA	300
GCGCGCGCGC GTGCGCGGCC AGGTGCTGGG GGTGTGCGCG GCGCAGCGCT CCGCGCGGAC	360
GCGCGCAAAA CGACCGCTCA CGCAGCTGGG TCCCGCTGGC ATATCCCTTG CGGTCTCTGG	420
CGATATTGGA CCGCATGCC CCGACCGCGT ACAGGCGCGC CACGACCG	468

(2) INFORMATION FOR SEQ ID NO:175:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGTAAAG GCGGGCAGGG TGGCATCGGC GCGCGCGCGG AGAGAGGGGC CGACGGCGCC	60
GGCGCCCAATG CTACCGCGGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC	120

GGCGGCGCGG GCGGCAATGG CGGCGCGGGC GSCAACGCGC AGGCGGCGCG GTACACCGAC 180
GGGCGCACGG GCACCGGCGG CGACGGCGGC AACCGCGGC 219

(2) INFORMATION FOR SEQ ID NO:176:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGCGCGCA AGGCGCGCGA CGGTGGCCAC GCGGTGAGC GCCTCGGCGG 60
CAACAGTTCC GTACCCCAAG GCGGCGCGCG CGGTGGCGGC GCGGCGGCGG GCGGCGGCGG 120
CAACGCGCTT TTGCGGCGCA AGGCGCGGCTT CGGCGCGCAC GCGGTGAGC GCGGCGGCGA 180
CGGCGGCGGT ACCGTGCGCA CCGTGGCGCG TGGCGGCGGC AACGGCGGTC TGGCGGCGCG 240
GGGCGGCGGC GCGGTCTTTG CCGGTGCGCG CGGCGCGGCG GCGGTGAGTC GCGAGGCGCG 300
CAAGGCGGCG GCTCCACCG GCGGCAACGG CGGCTTGGC GCGGCGGCGG GTGGCGGAGG 360
CAACGCGCGG GCTGTCGCG AATCGGCGCT GACCATGAGC AGCGCGGCGA AGTTGCGTGC 420
CATCGCATCA GCGGCGTACT GCGGCGAACA CCGGGAACAT CACCGGAGTT AGCGGGGCGC 480
ATTCTTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCGGCTGG TGGCGGCGCG CAGCTCTTCA GCGGCGGAGC CGCGCGGCGT GCGCTTGGGG 60
TTGGCGGCAC GCGGCGCGAG GGTGGGCGTC GCGGTGCGCG AGCGGCGGCG GCGGAGCGCT 120
CGGCGGCGAC AGGTCTAACC GGTGGTACCG GGTGCGCTGG CGGCGGCGCG GCGGTGCGCG 180
GCCAGAGCGG CAACGCCATT GCGGCGGCGA TCAACGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CGGGGCCCC GCGGGTGGTG GCGGGGCGGG CCACTACAAAT TTCCAACGGC	60
GCGCAGGGTG GTGCCGCGGG CCAAGGCGGG CAAGGGCGGG TGGCGGGGGC AAGCACCACC	120
TGATCGGGCT AGCGGCACCG GGGAAAGCGG ATCCAACAGG CGACGATGCC GCGTTCCTTG	180
CCCGGTGGGA CCAGGCGGGC ATCACTAGG CTGACCCAGG CCACGCCGTA ACGGCCGCCA	240
AGGCGATGTT TGGCTGTGT GCTACCGGGG TACAGGTCT ACAGCTGGTG GCGGACCTGC	300
GCGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTGGCTGCC ATCGCATCAG	360
GCGGCTACTG CCGCGAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:178:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAGGCGGG CACCGCGGGG GCGGCGATGA ACAGGCTCGA CCGGCTGCTA GCGGCGCAG	60
ACGGCGGCGA AGCGGCGACC GCGGCGACCG GCGGCAACGC CCGCGCGGGC GGCACCACT	120
TCACCGAAGG GCGGCGAGGC AACGCGGCGA ACGGCGGTGA CCGCGGGGTC GCGGCGAACG	180
GCGGAACCGG CGGAACCGGG GCGGCAACCA CCGGCGACCG CCGCGCGGGC ACCACAGCGG	240
GCGACGCGGG GCGCGCGGGG GCGGCGGGAA CCGGCGGAAC CCGCGGAGGC GCGGCGACCG	300
GCAACGCGGG CCGACAGGCG AACGCGGGCA ACGGCGGCGC CCGCGGCAAA GCGGCGACCG	360
GCGGCGACCG TGCACTTCTA GCGGCGACCG GTGGTGCGGG	400

(2) INFORMATION FOR SEQ ID NO:180:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GCGACGCGGG GCAACGCGGG CATGCGCTGC ATTGGCGGGC AACGCGCTTC GCGGACGCGC	60
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AGCGGCAACG GCGGCCAAGC GCGGCAGCGG CGGCAACGCG GCGCAACGCG GCATGGGCGG	120
CAACAGCGGC ACCGGCAGCG GCGACGCGCG TGCGCGCGGG AACGGCGCGG CCGCGGGCAC	180
GGCGCGCACC GCGCGGAGCG GCGGCGTCAC CGGTACTGCG GCGACGCGCG GCAGCGGTGG	240
CACCGCGCGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC	300
GCAGCGCGGG GGTGACCGTG GCAACGGCGG CGACGGTGCG TTGCGCGCGG GGGCGCGGGC	360
CGCGCGCGGT GCGTTGACCG CTGGCGGCAA CGGCAACGCG GCGCAAGGCG GCGCGCGCGG	420
CGATGCGCGG AACGGGGCCA TCGGCGGCCA CGGCGGACTC ACTGACGACC CGGCGGCGCA	480
CGGGGGCACC GCGGCGAAGC GCGGCACGCG CGGCACCGCG GCGCGCGGCA TCGGCAGC	538

(2) INFORMATION FOR SEQ ID NO:181:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCGCGTGG TGCGCGCGGC CAGCTCTTCA GCGCGGAGG CGCGCGCGGT GCGCTTGGGG	60
TTCGCGGCAC CGCGCGCCAG GGTGGGCTG GCGGTGCGCG AGCGCGCGCG GCGCAACGCG	120
CGCGCAGCAC AGGTCTAACC GGTGTACCG GCTTGGCTGG CGGCGCGCGC GCGCTGCGCG	180
GCGACGCGCG CAACGCGATT GCGCGCGGCA TCAACGCTC CGGTGGTGGC GCGCGCACC	239

(2) INFORMATION FOR SEQ ID NO:182:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 988 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGGCG CGGTTTCGCC GCGCGCGCGG GCGGAGAAGG CGAGCGGGCG	60
GGCAACAGCG GTGTGGGCGG CACCAACGCG TCGCGCGCGG CGCGCGGTGC AGCGCGCAAG	120
GCGCGCAGCG GAGGTGCGCG CGGTCGCGCG GCGGACAACC CCACCGGTGC TGGTTTCGCC	180
GGTGGCGCGG GCGGCAACAG TCGCGCGCGG GCGCGCGCGG GCGCGCGCGG GCGGACCGGT	240
ACCGCGCGCA CGCGCGCGCT TGTGCGCGCG ACCGCTAGTG CAGGCATGCG CGGCGCGCGG	300
GGCGCGCGCG GTGACGCGCG CGATGGGCGG AGCGGTCTCG GCGTGGCGCT CTCGCGCTTT	360

GACGGGGGCC AAGCGGGCCA AGCGGGGGCC GGCGGCAGCG CCGGCGCGGG CGGCGTCAAC	420
GGGCGCGGCG GGGCGGCGCG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCGGCA	480
GGTCTCGGCG ACAACGGCGG GGTGCGCGGT GACGGTGGGG CCGGTGCGGC GCGCGGCAAC	540
GGCGGCAACG GCGGCGTGGG CCGGACAGCC AAGGCGGCGG ACGGCGCGGC GCGCGGCAAT	600
GGCGGCAACG GCGGCGCGCG CCGTCTGTGC GGGCGCGGCG ACAACAATTT CAACGGCGGC	660
CAGGGTGGTG CCGCGCGGCA AGGCGGGCAA GCGGCGTTGG GCGGCGCAAG CACCACTGTA	720
TGGCGGTAGC CGCACCGGGG AAGCGCGATC CAACAGCGGA CGATGCGCGC TTCTTGGCGG	780
CGTTGGACCA GCGCGCGATC ACCTACGCTG ACCCGGGCCA CGCCATAAGC GCGCGCAAGG	840
CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGATCGCG GACCTGCGGG	900
AATACAATCC CCGGCTGACC ATGGACAGCG CGCGCAAGTT CCGTGCATC GCATCAGGCG	960
CGTACTGCCC CGAACACCTG GAACA	985

(2) INFORMATION FOR SEQ ID NO:183:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCG CGCGGCATCG GCAGCTGCGG ATTGCGCGGG TTTCGCCACC	60
CGAGGAAGAAG CGGTACCAGA TGCGGCTGCG GAAGTAGGGC GATCGGTTGG CGATGCGCGC	120
ATGAACGGGC GGCATCAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACCGTG GATCAGCAAG	240
AGATTATTGAA GAGGCGCAAC GAGGTGGAGG CCGCGATGGC GGACCCAGCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGCGCGCTA AAAACGCGCG CCAACAGCTG GTATTGTCCG	360
CCGACACATC GCGGGAATAC CTGCGGCGCG GTGCCAAAGA GCGGCGAGGT CTGCGGACCT	420
CGCTGCGCAA CGCGGCGAAG GCGTATGGCG AGGTTGATGA GGAGGCTGGG ACCGCGCTGG	480
ACAACGACCG CGAAGGAATC GTGCGGCGAG AATCGGCGCG GCGGCTCGGA GCGGACAGTT	540
CGGCGGAATC AACCGATAGC CCGAGGCTGG CCACGCGCGG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAGGGAAG CTCGAACCGG GCGACCAAGG GGCATGCTGC GCGGACCTTG	660

CEGATGGGTG GAACACITTC AACCTGAGCG TGCAAGCCGA COTCAAGCGG TTCCGGGGGT	720
TTGACAACTG GGAAGGCCAT GCGGCTACCG CTTGCGAGGC TTGCTCGAT CAACAACGGC	780
AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGCG CAAGCAGGCT CAAATATGCG	840
CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG	900
AACGGCTTTA CCGGAAAAAC CCTTGGGCCC GCGACCAAT TCTCCCGGTG TACCGGAGT	960
ATCAGCAGAG GTGCGGAGAG GTGCTGACCG AATACACAA CAAGGCAGCC CTGGAACCGG	1020
TAAACCCGCC GAAGCCTCCC CCGCCCATCA AGATCGAGCC GCGCCCGGCT CCUCAAGAGC	1080
AGGGATTGAT CCGTGGCTTC CTGATGCCCC CGTCTGAGCG CTCGGGTGTG ACTCCGGTA	1140
CGGGGATGCC AGCGGCACCG ATGGTTCGCG CTACCGGATC GCGGGTGGT GCGCTCCCGG	1200
CTGACACGCG GCGGCAGCTG ACCTCGGCTG GCGCGGAAGC CGCAGCGCTG TCGGGCGAGC	1260
TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGAGGCGCG CGGGGTGGCG TCGGCGCGGT	1320
TGGGATCCCG GATCGGGGGC GCGGAATCGG TCGGGCCGCG TGGCGCTGGT GACATTGCCG	1380
GCTTAGGCCA GCGAAGGCCG GCGCGCGGCG CCGGCTGGG CGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGTTCT CAGCAGGAAG	1500
ACGAGCGGCT CTACACCGAG GATCGGGCAT GGACGAGGC CGTCATTGGT AACCGTCGGC	1560
GCCAGGACAG TAAGGAGTCG AAGTAGCAT GGACGAATTG GACCTGCATG TCGCCCGGGC	1620
GTTGAGCTG GCGGCGCGGT TCGAGTCGGC CTTAGACGGG ACCTCAATC AGATGAACAA	1680
CGGATCTTC CCGCCACCG ACCAAGCCGA GACCGTCGAA GTGAGCATCA ATGGGCACCA	1740
GTGGCTCACC GACTTCCCA TCGAAGATGG TTGCTGAAG AAGCTGGGTG CCGAGCGGCT	1800
GCTGAGCGG GTCAACGAGG CGCTGCACAA TCGCAGGCC GCGGCTCGG CTTATAACGA	1860
CGCGCGGGCG GAGCAGCTGA CCGCTCCGTT ATCGGCCATG TCCCGCGGGA TGAACGAAGG	1920
AATGGCTTAA GCGCATTTGT GCGGTGGTAG CGACTACGCA CGGAATGAGC GCGCAATGC	1980
GGTCATTGAG CGGCGCCGAC ACGCGGTGAG TACGCATTGT CAATGTTTTG ACATGGATCG	2040
GCGGGTTGCG GAGGGCGCCA TAGTCTGGT GCGCAATATT GCGGCAGCTA GCTGTCTTTA	2100
GCTTGGTTA CGCTGGTTAA TATGAGCTC CGTTACCA	2138

(2) INFORMATION FOR SEQ ID NO:184:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 460 amino acids
 (B) TYPE: amino acid

(C) STRADEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

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Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1           5           10           15

Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20           25           30

Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
 35           40           45

Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50           55           60

Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
 65           70           75           80

Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85           90           95

Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100           105           110

Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115           120           125

Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130           135           140

Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
145           150           155           160

Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
165           170           175

Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
180           185           190

Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
195           200           205

Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
210           215           220

Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
225           230           235           240

Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
245           250           255

Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro
260           265           270

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Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285

Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300

Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320

Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335

Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350

Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val
 355 360 365

Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380

Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400

Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415

Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430

Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445

Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(C) INFORMATION FOR SEQ ID NO:185:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15

Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30

Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45

Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270
 Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:186:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

- (A) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(3) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

[illegible]

123 INFORMATION FOR SEQ ID NO: 188:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(X): SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr
1 5 10 15
Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys
20 25 30
Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr
35 40 45
Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly
50 55 60
Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu

179

65	70	75	80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala	85	90	95
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala	100	105	110
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly	115	120	125
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly	130	135	140
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn	145	150	155
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala	160	165	170
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val	175	180	185
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp	190	195	200
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu	205	210	215
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser	220	225	230
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe	235	240	245
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu	250	255	260
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp	265	270	275
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp	280	285	290
Arg Asp Val Ile Val Ala Asp	295	300	305
	310		

(2) INFORMATION FOR SEQ ID NO:189:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3072 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCCTA TTCCGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAATCAA CAGCAGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCTTG AATGAGGGCC GCGGCGACTT CTTCGCGGTG GTACCGAGCC	180
TGGCGGTATT GGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTGGCG TTGAACAAGA	240
ACCTTCGGGA GTTCAACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTGG AACGCCATCC	300
AGCAATTGGA CAGCTTGGTC GCGGTGCGCC GCGCGTTCTT CGCCAGAGAC CGCGAGGTCC	360
TGACCGATGA CGTCAATAAT CTGCGGACCG TGACCAACAC GTTGTGTGCG CCGGATCGGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCGACGCT GCGCGCGAAC ATTAACCAAC	480
TTTACCATCC GACACACGGT GCGTGGTGT GCTTTTCCGC GTTCAAGAA TTGCGCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTGAGG CGGGTAGCGG GCTCGGTAT CAGAGTCCG	600
CGGAATCTG TGCGCACTAT CTGGCGCCAG TCGTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCCGGCT GAACGTGGCC AGCACCGCT CGACACTGCC TAAAGAGATC GCGTACTCG	720
AGCCCGCGTT GCAGCCCGCC AACGGGTACA AGGACACCAAC GGTGCCCGGC ATCTGGGTGC	780
CGGATACGCC GTTGTACAC CGCAACACGC AGCGCGTTG GGTGGTGGCA CCGGGATGC	840
AAGGGGTCCA GGTGGGACTG ATCAGCGCAG GTTTCTGAC GCGGGAGTCC CTGGCCGAAC	900
TGATGGGTGG TGCGGATATC GCGCTTGGT GGTGAGGCT GCACACCGCC CCGGACCTCC	960
CGAATGGCTA CGACGAGTAC CCGGTGCTGC GCGGATCGG TTACAGGCC CCGCGGTTC	1020
CGATACCAGC GCGCGTCTCT GCGCGGACG TAATCCCGGG TCGGGTGGCA CCGGTCTTGG	1080
CGCGGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AAACCTGAC TACATGGGCC	1140
TCTGTGTGCT CTCGCGCGGC CTGGCGACCT TCGTGTTCGG GGTATCATCT AGCGCCGCCC	1200
GTGGAACGAT GCGCGATCGG CAGCTGTTGA TACCGGCGAT CACCGGCTG GGTGTGATCG	1260
CGGCTTCTCT CGCAGATTCC TGGTACCGGA GAGAAGATCC GCTCATAGAC ATCGCTTGT	1320
TCCGAGACCG AGCGGTGCGG CAGGCCACCA TGACGATGAC GGTGCTCTCC CTCGCGCTGT	1380
TTGGCTGCTT CTCTCTCTTC CCGAGCTAGC TCCAGCAAGT GTTGACACAA TCACGATGC	1440
AATCGGGGCT GCATATCATC CCACAGGCCC TCGGTGCCAT GCTGCGGATG CCGATCGCCC	1500
GAGCGAGCAT GGACCGACCG GGACCGGCGA AGATCGTGTCT GGTGGGATG ATGCTGATCG	1560
CTCGCGGCTT GCGCACCTTC GCGTTGGTGG TCGCGCGGCA AGCGGACTAC TTACCGATTG	1620

TCGCGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCATGATG CCATGTGCG	1680
GGGCGGCAGT GCGACCCGTC GCGCCACATC AGATGGCTCG CGGTTCGACG CTGATCAGCG	1740
TCACCCAGCA GGTGGGGGGT TCGATAGGGA CGCACTGAT GTGGTGGCTG CTCACCTACC	1800
AGTTCATCA CAGCGAAATC ATGCTACTG CAAAGAAAT CGCACTGACC CCAGAGAGTG	1860
CGCGCGGGCG GGGCGCGCG GTTGACCCCTT CCTGGTACC GCGCCAAAGC AACTTCGCG	1920
CGCACTGCT GCATGACCTT TCGCAGGCT AGCGGTGGT ATTGGTGATA GCGACCCGCG	1980
TAGTGGTCTC GACGCTGATC CCGCGGCGAT TCGTCCGAA ACAGCAGGCT AGTCATCGAA	2040
GAGCACCGTT GCTATCCGCA TGACGTCTTC TT	2072

(12) INFORMATION FOR SEQ ID NO:190:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1923 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA GAAGTCGTTT GTGACGACC TGGACATCGA CTGCTGTCTG ATGTTGAGA	60
TGCGGTGCA GACCGAGGAC AAGTACGGCG TCAAGATCCG CGACGAGGAC CTCGCGGCTC	120
TGCGTACGCT CGGTGACCTT GTGCGCTACA TCCAGAAGCT CGAGGAAGAA AACCCGAGG	180
CGGTCAGGCT GTTGGCGGCG AAGATTGAGT TCGAGAACCC CGATCGCGCA CGACGAGTC	240
GGTGGCTTC ACCGACATCG GAGGTCGAG ACGCGGCTCG TCGCTGTGCA CGTCACGCCA	300
GGTTGGCGTG TCGCGGCTT CAGCAAGTG TTCCACGAC ACGAAGGGAG CTTGCGGAAA	360
GGTGACTGAT CCGCGACCA CATAGTGAT GCGACCTGCG CTGACAATTG CGCGGGTCC	420
GAGTTGGCG GCGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GCGCGCGGCG	480
CGGCTGGCT GGTGTTTTGG GCGCGCGGAT GCGCACGAGC AGAAGCAGCA TCGCGGGGAT	540
GAACAGCGCC ACGGCAATCA CGACGAGCAG ATTTCGACG CATACCTCTC CGTACCGCTG	600
CGCGCGGCTT GGTGATCGG TCGCATATCG ATGGCGCGCT TTAACGTAC AGCTTTGCGG	660
GGACCGCGGG TCACACCGGG CGAGTTGTCC GCGCGGGAAC CCGGCAAGTC TCGCGCGGCG	720
TCACCCGAGC TGACTGGTGC ACCATCCGGG TGTGGGTGAC CGTGCAACTC AAACACACTC	780
AACGGCAAGC GTTGTGAGG TCACGAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC	840

GACCCGCGGC AGGTGCGGAG TCACGAGCTT TGCGCGGCA GCTTTCGCGG TGAAGCGAC 900
 CAGGGGATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGCT CGGTCAAGGC 960
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGAG GTGATGTCG CCAAGTAGGC 1020
 GTGGACGGCA ACAGGGGCAA TACGATCGCG CGGTGCTAGC CGGTCAADA CCGAATAGGT 1080
 TTCCACAGGC CGGTGCGGCA TCAGATGGAC GCCACGGTTC AGCGCGCGCA CGCGGCGCTC 1140
 GTGCGCTTTC TGCCAGGTGC CGAATCGGCG AACGAGCAG CTGGTGCTCT GTGCGATCAC 1200
 CGCGCTGTGC GATCGAGGCT TTCCGAAACG ATTTCGTGCG TCAACGGGCG CAGGGGAGCT 1260
 TCTGCGCGTG CGACGAGAAC CGAGCTTCC CGAAGGAGTT CGACACGCTT CGGGGCGGCG 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCGACCT GGTGCTTCCC GCGCAAGCCA 1380
 AGCGCGTTCG GAATCGGCTT GGAATCACC AGACUTCTTG CGACATCGAT GGTGTTCTGC 1440
 ATGTTAGSAA ATTACCATC GCACGTTCCA TAGCGGTGTC CTGCGCGGGA TGTGGGAGC 1500
 ATCGCTTAGC GTATCGAAGC ATTGTTTCGG AATGGCTGA GGGAGCGTGC GGTGCGGCTG 1560
 ATGGGTGTCG ATCGCGGCTT GACCGGATGC GCGCTGTGCG TCATCGAGAG TGGCGGTGGT 1620
 CGGCGCTCA CCGCGCTGGA TGTGACGTC GTGCGCACAC CTGCGGATGC GCGCTTGGCG 1680
 CAGCGCTTGT TGCCCATCAG CGATCGGCTC GAGCACTGCG TGGACACCCA TCATCGAGAG 1740
 GTGGTGCTTA TCGAACGGT GTTCTCTGAG CTCACCTGTA CCGCGGTGAT GGGCACGCGC 1800
 CAGCGCTGCG GGTGATGCTC GTGCGGCGCG GCGAAGCTG GTGTGAGCTT GCATTTCAT 1860
 ACCCGAGCG AGGTCAAGCG GCGGCTCACT GCGAAGCTT CCGCAGACAA GGTGAGGTC 1920
 ACC 1923

(1) INFORMATION FOR SEQ ID NO:191:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCTGTCG AGTGTCAAGC GCGATATGAG GTGCGCATTC AATTTCGCGG CCGCGCGGGA 60
 CGGTTGCGCA CCGAATCTCG AGCACCAGGT CCGTCAATTG CCGAAGGTGC CCAAGTGCCT 120
 GCGCAATGTC GTGCTGGGTT TCTTGAACGA AGGCGTGGCG TATGGGTTGC CCTACCCCCA 180
 AACACGCCCA GTCCAGGAAT CCGTCTCGCG GCGGCGGATT CCGAGCGGCA TGTGCTAGCC 240

GCGGATGGTT CAGACGTAAAC GGTTCGGCTAG GTCGAAACCC GCGCCAGGSC CGCTGGACGG	300
GCTCATGGCA GCGAAATAG AAAACCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG	360
AGTGCTTGGT GGTTCGTGTT TAGCCATTGA GTGTGGAGT GTTGAGACCC TGGCTTGAA	420
GCGGACAACG TGCTTTTGCC TCTTGGTCCG CTTTTCGCG CCGACGCGGT GGTGGCGAAA	480
GCGGCTGAGT CCGGAATGCT CCGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG	540
CCACCCGATG ATTATGACCA CTGGGCGGCT GCGCGGAGG ACGGCGCGCA TGTGATGTC	600
CAGGCGCGCG AAGGGCGGGA GCGAGAGGCC GCGGCCATGG ACGAGTGGA TGAGTGGCAG	660
GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGAGTAGC	720
AGCAGCTGA TTCCGATTG TCCGCGCGCC GGTAGGAGA GGGGCGCAG ACTGCTTTA	780
TTTGACCAAT GATCGCGCT CTCGGTGTTC CCGCGCGCG GTATGACAC AGTGAATGTG	840
CATGACAAGT TACAGTATT AGGTCCAGT TCAACAAGGA GACAGCGAC ATGGCAACAC	900
GTTTATGAC GGTTCGCGAC GCGATCGCGG ACATGGCGGG CGSTTTTGA GTGACGCGCC	960
AGAGGTTGGA GGACGAGGT CCGCTGATGT GGGGCTCCCG GCAAAACATC TCGGGNGCGG	1020
GCTGGAGTGG CATGGCGAG GCGACCTGGC TAGAC	1085

(2) INFORMATION FOR SEQ ID NO:192:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CGGCTGCTGT GTTGGCATAC TCGGCTGCGG CCGCTCGAC CGGACTGGCC GTGGCTGTG	60
TCGGGGGTGA CCACCGGGAT CCGGGAACCA TCCGAGTCA CTTGGCAATG ATCCACCTCG	120
CGGAGCTGGT CACCCAGCCA CCGGCGGTTG TCGACAGCG CTTGCATCAC CTTGGTATAG	180
CGGTGCGGCC CCGGCGCGAG GAAGTTTAG TACTGGCCCA CCACCTGCTT ACCGGGACGG	240
GAGAATTCA GGTGAAGGT CCGCATGTG CCGCGAGGT AGTTGACCGG GAAAGCAGA	300
TCTTCGCGCA GTTGCTCGGG CCGGCGCGAC ACGACAAACC CGACCGCGGG ATAGGTCAG	359

(2) INFORMATION FOR SEQ ID NO:193:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

AACGGGCGCG	TGGGACAGCG	TCCTCTAAGG	GCCTCGTTG	GTGSCATGAA	GTGCTGGAAG	60
GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCGCG	TAGTCTTAGT	CCGAGTCGCC	120
CGCAAAGTTC	CTCGAATAAC	TCGGTACCGG	GAGCGCCAAA	CCGGGTCTCC	TTGCTAAGC	180
TGCGCGRACC	ACTTGAGGTT	CGGGGACTCC	TTGACGTCCA	GACCGATTCC	TTGCGATGAC	240
TSATCGGTTG	GCCGCGCTGG	CGCGAATCCG	CGCCCGAGCG	GGGTGATGTC	AACCCAGTGG	300
GTGSCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATGGA	GGACTTCTCC		350

(12) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Glu	Gln	Pro	Lys	Gly	Pro	Phe	Gly	Glu	Val	Ile	Glu	Ala	Phe	Ala	Asp	1	5	10	15
Gly	Leu	Ala	Gly	Lys	Gly	Lys	Gln	Ile	Asn	Thr	Thr	Leu	Asn	Ser	Leu	20	25	30	35
Ser	Gln	Ala	Leu	Asn	Ala	Leu	Asn	Glu	Gly	Arg	Gly	Asp	Phe	Phe	Ala	40	45	50	55
Val	Val	Arg	Ser	Leu	Ala	Leu	Phe	Val	Asn	Ala	Leu	His	Gln	Asp	Asp	60	65	70	75
Gln	Gln	Phe	Val	Ala	Leu	Asn	Lys	Asn	Leu	Ala	Glu	Phe	Thr	Asp	Arg	80	85	90	95
Leu	Thr	His	Ser	Asp	Ala	Asp	Leu	Ser	Asn	Ala	Ile	Gln	Gln	Phe	Asp	100	105	110	115
Ser	Leu	Leu	Ala	Val	Ala	Arg	Pro	Phe	Phe	Ala	Lys	Asn	Arg	Glu	Val	120	125	130	135
Leu	Thr	His	Asp	Val	Asn	Asn	Leu	Ala	Thr	Val	Thr	Thr	Thr	Leu	Leu	140	145	150	155
Gln	Pro	Asp	Pro	Leu	Asp	Gly	Leu	Glu	Thr	Val	Leu	His	Ile	Phe	Pro	160	165	170	175

Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 195 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

435	440	445
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln		
450	455	460
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro		
465	470	475
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met		
485	490	495
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile		
500	505	510
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp		
515	520	525
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met		
530	535	540
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala		
545	550	555
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln		
565	570	575
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr		
580	585	590
Glc Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu		
595	600	605
Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser		
610	615	620
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser		
625	630	635
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser		
645	650	655
Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg		
660	665	670
Arg Ala Pro Leu Leu Ser Ala		
675		

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
1           5           10           15
Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
20           25           30
Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
35           40           45
Tyr Ile Gln Lys Leu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
50           55           60
Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
65           70           75           80
Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
85           90           95
Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
100          105          110
Thr Arg Arg Asp Pro Arg Glu Arg
115          120

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(2) INFORMATION FOR SEQ ID NO:196:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
1           5           10           15
Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
20           25           30
Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
35           40           45
Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
50           55           60
Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
65           70           75           80
Gly Asp Gly Ser Asp Val Thr Val Gly
85

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(2) INFORMATION FOR SEQ ID NO:197:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
 1 5 10 15
 Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
 20 25 30
 His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
 35 40 45
 Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
 50 55 60
 Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
 65 70 75 80
 Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
 85 90 95
 Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
 100 105 110
 Pro Asp Ala Gly Ile Gly Gln
 115

(2) INFORMATION FOR SEQ ID NO:198:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
 1 5 10 15
 Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
 20 25 30
 Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
 35 40 45
 Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
 50 55 60

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
 65 70 75 80
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
 85 90 95
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
 100 105 110
 Glu Asp Phe Ser
 115

(2) INFORMATION FOR SEQ ID NO:199:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG CAATGCTTT GTGACAGAT GTGGATGCG GCCTGCTGC TGGGATGGC 60
 GTGAAGAGCG CCGAGTGTT CCGCGCATC GGGGAGAACA TGAAGTGT CAAAAGGCTG 120
 GTGGGCGCG CCATCATCG GTTGGCGAC GAGCGCAGT GCACGCACTG TCAACACCAC 180
 GCGGTGTTC GTTGGCGTT CAGCTGCCA TGAGGGTGT GCTGACCGG GCGGCGCGCT 240
 TCATCGGTC GCGCGTGAT GCGCGTTAC GCGCTGCGG TCACGACGTG GTGGGCGTCG 300
 ACCGCTGCT GCGCGCGCG CACGCGGCAA ACCCGTGCT GCGACCGGG TCGCAGCGGG 360
 TCGAGCTGCG CGACGCGAG GCGCTGCGG CTTTGTGGC CGGTGTGAT GTGGTGTGTC 420
 ACCAGCGCG CATGTTGGT GCGGCGTCA AGCGCGCGA CGCACCGCTG TATGCGCGCC 480
 ACAAGGATT CGCGACGAG GTGCTGCTG GCGAGATTT CCGCGCGCG GTCCGCGCTT 540
 TGTGCTGCG GTGCTGATG GTGTTTACG GCGAGGCGG CTATGACTGT CCGCAGCATG 600
 GACCGGTGCA CCGGCTGCG CGCGCGGAG CCGAGCTGGA CAATGGGTC TTGAGGACCC 660
 GTTCCCGCG GTGCGCGAG CCACTCATCT GCGAATTGCT CGACGAAGAT GCGCGTTGC 720
 GCGCGCGAG CTTTACGCG GCGCAAGAC CCGCAGGAG CACTACGCG TGGCTGCTG 780
 GGAACGAAT GCGGTTCCG TGGTGGCGTT G 811

(2) INFORMATION FOR SEQ ID NO:200:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCCAT GTGGCCGAGC ATGACTTTCC GCAACACCGG CBTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTGGCC GTTGTTCAGC GTCCACCCGT	120
GCTCGGACGC GGAACCCATG CTTTCAACGT AGCCTGTCCG TCACACAAGT CGCGAGCGTA	180
AGCTCACGGT CAAATATGCC GTGGAAATTC GCCGTGACCT TCCGCTCCGC GACNATCAG	240
GCATACTCAC TTACATGCCA GGCATTTGGA CGGTTTGGAT CGCCTTCGGG CTGGTGAACG	300
TGCCCGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGTTTCCAC CAGGTGCACG	360
CCAAAGACAA CGGACGCATC CGGTACAAGC GCCTCTGCGA GCGGTGTGGC GAGGTGGTGG	420
ACTACCGCGA TCTTGCCCGG GCTTACGAGT CCGCGGACCG CCAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CTTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTCC	540
TCCCGCGCGC CGAGCTGGAC CGGATGATGT TCGACCGCAG CTACTTTTTC GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTCTCTCTGG CTAGACACT CGCCGAGCC GACCGGATGG	660
CGATGTGTGA TCGCCGCCAC GCGCGTGAAT CGAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TGGCGTCTGA GCTCGGCTAC CACAAACGGT AGAAGCATCG AGACATTCGC GAGCTGAAGT	780
GGCGCGCTAT AGAAGCGGCT CTGCGCGATT ATCAACGGCA AATACGCTT ACTCATGCCA	840
TGGCGCGTGC TCACCGGATG CGAGCTTTTC GCGACGTCGC ACTCGCTGCG GCGGACCTC	900
AAGTGGGLAT GCTCCGCCAC GCTTCCCGGA AACCGGTTCC GCGGGGTCCG CTCATGGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CGGCACCGCC GGCATACGC CGAGCGGCAC CGTTACCGCC GTTTCGCGCG TTGCCCCCGT	60
TGCGCGCGGT CGCGCGCGCC CGCGCGATCG AGTTCTCATC GCCAAAAGTA CTGCGCGTGC	120
GACCGGAGCC GCGCTTGGCG CGCTCACCGC CAGCGCGCGC GACTCCACCG GCGCCACCGA	180

CTCCGCGGCT GCCACGGTTC CGCGGTTGC CGATCAACAT GCGGCTGCGC CCACCGTTGC	240
CACCCGCGCC ACCGCGTCGC CCCACCGCGC CGACACCAAG CGAGCTGCGC CCGGAGCCAC	300
CATCACCAAC TACGCGACCG ACCGCGCAGA CACCAGCGAC CGGCTCTTGC TGAACGTCGC	360
CGGTGCGACC ACGCGCGCGC TACCGGCCAA CCGCACCGGC AACCGCGCGC CGGCATCCCG	420
CGCGCGCGCC GCGGTTGCGC CGTTGCGCGC CGTTGCGGAA CAACACCGCG CCGCGCGCGC	480
CGTTGCGCGC CGCGCGCGCG GTCCGCGCGC CGCGCGCGAC GCGAGGCGCG CTGCGCGCGT	540
TGCGCGCGAT ACCACCGTTG CGCGCGACCA CATCGGTTG TGCGCGCGCG TCTCGCGCGT	600
CGAACCTGCG GATCGCGCGC TTGCGCGCGC TTCCCGCGCG CCGCGCGCGT CGCGCGCGTAC	660
CACCGATACC ACCCGCGCGA CGCGCGCGAC CGTTGCGCGC ATCAGCGAAT AGCACCGCGC	720
CGCGCGCGAC ATTGCGCGCA GTCGCGCGCG CGCGCGCGTC GCGCGCGGAG CGCGCGACTG	780
CAGCGCGGTT ACCACCGAAA CGCGCGCGTAC CACCGGTAGA GCGCGCGGAG CGCGCGTGTG	840
CGAAAGCGCG GCGTCCGCGC CGCGCGCGTAC CACCGCGACT GCGCGCGGCT ACACCGTGGC	900
ACCGGTTGCG ACCATCACCG CGAAGCGCGC TGCGAATGTC GCGCGCGCGC ACTCGCGCGT	960
CGCGCGCGTT GCGCGCGCGC CGACCGCGAG CGCGCGTACC GCGCGTACCA CCGCGCGCGC	1020
CGGTGCGCGT GCGCGAGGCT GCGCGCGCGC TGCGCGCGTC GCGCGCGGTC CGACCGTGGC	1080
GCGTCCGCGC AGTGGCGTGC CGCGCGCGTGC CGCGCGTGGC CGCGGTTTGA TCACCGATGC	1140
CGGACACATC TGCGCGCGTC TGCGCGCGTGC TGCGCGCGCG GCGCGCGGTC GCGCGCGGTC	1200
CGTTTGGCGC GCGCGAGGCG GCGCGCGCGC TACCGCGCGC GCGCGCGTGC CGGAACGCGC	1260
CGCGGTTGCG GCGGTACCG CGCGCACCGC CGATGCGTGC GCGCGCGTGC GTGCGCGCGA	1320
CACCGCGGTT GCGCGCGGTC CGCGCACCGC ACCCGCGGTT CGCGCGCGCA CCGCGCGCGC	1380
CGCGCGTACC ACCCGCGCGC CGTTGCGCGC CGTTGCGCGT CAACCGCGCG GCGCGCGCGC	1440
TGCGCGCGGT TTGACCGAAC CGCGCGCGCG CGCGGTTGCG ACCGTTGCGA AACAGCGAGC	1500
CGCGCGCGCG GCGAGGTCGC CGCGGTCGCG TGCGGTCGCG GCGGTTGCGC ATCACCGCGC	1560
GCGCGAAGAG CGCGCGGTC GCGCGATTCA CGCGACCGAG CAGACTCGCG TCACAGCGCG	1620
CTTCACTGCT GGCATACCGA CGCGCGCGCG CAGTCAACCG CTGCGACGAG TGCTGCTGAA	1680
AGCGTGGCAC CTGTACGCGT AGCGCGTGTG ACTGCGGAGC ATGGCGCGCG AACACCGCGC	1740
CAATCGCGCG CGCACTTCA TGCGGAGCGC CAGCGACCGC TTGCGTGCCT GCGGTCGCGC	1800
CGCGCGCGAT AGCGCGCGTC ACCTGCGAAG CAGTACTGGA TAAATCCAAA GCGCGCGTTC	1860

CCAGCAGCTG CGGCGTGGCG ATCACCAGAG ACACCTGSCA CCTCCGGATA CCCCATATCG	1920
CCGACCCGTG TCCGACGCGG CCACGTGACC TTGGGTGGCT GGCTGGGGGC CCGACTATG	1960
CCCGCGAAGG CCTCGTTCTT GATTGGCCCC GCGCGGCAGC TTGTGGGCG AGTTGAAGAC	2040
GGGAGGACAG GCGGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGCGG	2100
AGATGAATAG GCGGACGCGG ATCTCCTTGT TGCTGAGTCC CTCACGACC AGTAGAGCCA	2160
CCTCAAGCTC TGTCGGTGTG AACGCGCCCC AGCCACTTGT CGGCGCTTTC CGTGACCGGC	2220
GGCCTCGTTC CCGGTACGCG ATCGGCTCAT CGATCGATAA CGCAGTTGCT TGGCGCCAGG	2280
CATGCTCGAA CTGCGTGTCA CCCATGGATT TTGGAAGGCT GGCTAGCGAC GAGTTACAGC	2340
CCGCGTGATA GATCGGGAAG CGGACCG	2367

(2) INFORMATION FOR SEQ ID NO:202:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln	Pro	Ala	Gly	Ala	Thr	Ile	Ala	Ala	Ser	Ser	Pro	Cys	Ala	Thr	Val	1	5	10	15
Gly	Ala	Gly	Gly	Gly	Thr	Gly	Ser	Pro	Val	Thr	Thr	Glu	Thr	Ala	Ala	20	25	30	
Thr	Thr	Gly	Arg	Gly	Gly	Ser	Gly	Asp	Val	Tyr	Glu	Ser	Ala	Ala	Ser	35	40	45	
Gly	Ala	Ala	Ala	Thr	Thr	Pro	Thr	Ala	Gly	Gly	Tyr	Thr	Val	Gly	Pro	50	55	60	
Val	Ala	Thr	Ile	Thr	Ala	Lys	Gly	Ala	Arg	Asn	Val	Ala	Leu	Arg	Asp	65	70	75	80
Ser	Ala	Val	Ala	Ala	Val	Ala	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Gly	Thr	85	90	95	
Ala	Val	Thr	Thr	Gly	Thr	Ala	Gly	Gly	Leu	Ala	Arg	Ala	Cys	Arg	Arg	100	105	110	
Gly	Gly	Thr	Val	Ala	Ala	Gly	Ala	Thr	Gly	Arg	Arg	Ala	Gly	Ser	Ala	115	120	125	
Met	Ala	Ala	Arg	Ala	Ala	Val	Ala	Ala	Gly	Leu	Ile	Thr	Asp	Ala	Gly	130	135	140	

His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365
 Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGCCAAACG CCGCGCGAT CCGCGCACG GAGGCGCGT ACGACCAGAT GTGGGCCCG	60
GACGTGGCG CGATGTTGG CTACCATGCT GGGGCTTCG CGGCGGTCTG GCGTTGACA	120
CGCTCGGCG AGCGCTGCG GACCGTGGG GCGGCGGGT CCGTGGTCAG CCGCGCGCG	180
GCTCAGGTGA CACCGCGGT CTTCGCGAC CTGGGCTTGG CGAACGTCCG CGAGGCGAC	240
GTCGCGAAC GTAATGTGG GAATTCAT CTGGGCTCG CCAACATCGG CAACGCGAAC	300
ATCGGCGCG GCAACATCG CAGCTCGAC ATCGGCTTGG GCAACGTGG TCTGGGTTG	360
ACCGCGCGG TGAACACAT CCGTTTCGG AACCGCGCA GCAACACAT CCGGTTTGG	420
AACCGCGCA GCAACACAT CCGGTTTGG AATACCGAG ACGGCAACCG AGGTATCGG	480
CTCAGCGTA GCGTTTGGT GCGGTTTGG GCGTGAAT CCGGCAACCG CAACATCGT	540
CTGTTCACT CCGGCAACCG AAGCTCGG ATCGGCACT CCGGTACCG GAACGTGGG	600
ATTGGCACT CCGGCAACG CTACACACG GGTTTTGGCA ACTCGGCGA CGGCAACCG	660
GCGTCTTCA ACTCGGAT AGCGACACG GCGCTGGCA ACGCGCGAA CTACACACG	720
GGTAGCTACA ACCCGGCGA CAGCAATCG GCGGCTTCA ACATGGGCGA GTACACACG	780
GGTACCTGA ACACGGCGA CTACACACT GCGTGGCGA ACTCGGCGA TGTACACAC	840
GCGGCTTCA TTAGTGGCA CTTCACACG GCGTTCTGT GCGCGGCGA CACCAAGG	900
CTGATTTGG GAGCGCGG GTTCTTCA CCGACACTG CCGGCTCGT GGGATCTTC	960
AACAGCGTG CCGGTAGCG CTCGCGTTC GTGAACCGG GTGCGACAA TCTGGCTTC	1020
TTCAACTCTT CCGCGGGCG CATCGTACG TCGGCGTGG CAACCGCGG CCGTCTGTA	1080
TGCGCGGTA TCACTCGG CACACCTTA TCGGTTTGT TCAACATGAG CCGGTGGG	1140
ATCACACCG CCGCTTGT ATCGGCGTTC TTCAACCGG GAGCGACAT GTCGGATTT	1200
TTGGGTGGG CACCGGTCT CAATCTCGG CTGCGAACG GCGGCTGCT GAACATCTC	1260
GCGACCGCA ACATCGGCA TTACACATT CTCGCGCGG GAAACGTGG TGAATTCAC	1320
ATCTTTGGC GCGGCAACT CCGCGCGAA AACATCTTG GACCGCGCA GTCGCGGCG	1380
TTCAATATG CGATGGGAA CATCGGATTA TTCAATGTG GTTCGGGAG CCGGGGAA	1440
TACACATCG CATCGGAAA CCGCGGATC TACACATCG GTTTTGGAAA CCGCGCGAC	1500
TACACATCG GCTTCGGAA CCGCGGCGC TTCAACCAAG GCTTTGCCA CCGCGCGAC	1560
AACACATCG GCTTCGGAA CCGCGCGAC AACACATCG GATCGGCGT GTCGCGGCG	1620

AACCAGCAGG	GCTTCAATAT	TGCTAGCGGC	TGGAACTCGG	GCACCGGCAG	CAGCGGCGTC	1680
TTCAATTGCG	GCACCAATAA	CGTTGGCATT	TTCAACGCGG	GCACCGGAAA	CGTGGGCATC	1740
GCAAACTCGG	GCACCGGGAA	CTGGGGTATC	GGGAACCCCG	GTACCGACAA	TACCGGCATC	1800
CTCAATGCTG	GCAGCTACAA	CACGGGCATC	CTCAACGCGG	GCGACTTCAA	CACGGGCTTC	1860
TACAACAGCG	GCAGCTACAA	CACGGGCGGC	TTCAACGTCG	GTAAACACCA	CACGGGCAAC	1920
TTCAACGTCG	GTGACACCAA	TACGGGCAGC	TATAACCCCG	GTGACACCAA	CACGGGCTTC	1980
TTCAATCCCG	GCAACGTCAA	TACGGGCGGT	TTGACACCGG	GCGACTTCAA	CAATGGCTTC	2040
TTGGTGGCGG	GCGATAACCA	GGGGCAGATT	GCGATCGATC	TCTGGGTCA	CAGTCCATTC	2100
ATCCCCATAA	ACGAGCAGAT	GGTCATTGAC	GTACACCAAG	TAATGACCTT	CGGCGGCAC	2160
ATGATCACGG	TCACCGAGGC	CTGGAGCGTT	TTCCCCCAAA	CTTCTATCT	GAGCGGTTTG	2220
TTCTTTCTCG	GCGCGGTCAA	TCTCAGCGCA	TCCACGCTGA	CGTTTCGAG	GATCACCTTC	2280
ACCATCGCGG	GACCGACGGT	GACCGTCCCG	ATCAGCATTC	TGGGTCTCT	GGAGAGCCCG	2340
ACGATTACCT	TCCTCAAGAT	CGATCGCGCG	CGGGGCATCG	GAAATTCGAC	CACCAACCCG	2400
TCGTTCGGCT	TCCTCAACTC	GGGCACGGGT	GGCAGATCTG	GCTTCCAAAA	CGTGGGCGGC	2460
GGCAGTTCA	GGCTCTGAA	CAGTGGTTTG	AGCGGCGCGA	TAGGGAATTC	GGGTTTCCAG	2520
AACCTCGGCT	CGCTCGAGTC	AGGCTGGGGG	AACCTGGGCA	ACTCGGTATC	GGGCTTTTTC	2580
AACACAGTA	CGGTGAACCT	CTCCACGCGG	GCCAAATGCT	CGGGCCTGAA	CAACATCGGC	2640
ACCAACTCTG	CGGGCTGTTT	CGCGGTTCCG	ACCGGGACGA	TTTTCAACGC	GGGGCTTGGC	2700
AACCTGGGCG	AGTTGAACAT	CGGACGCGCC	TCTGGCGGAA	TTGGGCACGA	GTTAGATACG	2760
GTTTCAACAA	TCATATCCGC	GTTTTCGCGC	AGTGCATCAG	ACGAATCGAA	CCCGGGAAGC	2820
GTAAGCGAAT	AAACCGAATG	GCGGCTCTTC	AT			2880

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15

Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
20 25 30

Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
35 40 45

Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
50 55 60

Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Gln Gly Asn
65 70 75 80

Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
85 90 95

Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
100 105 110

Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
115 120 125

Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
130 135 140

Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
145 150 155 160

Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
165 170 175

Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
180 185 190

Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
195 200 205

Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
210 215 220

Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
225 230 235 240

Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
245 250 255

Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
260 265 270

Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
275 280 285

Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
290 295 300

Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

305	310	315	320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn	325	330	335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly	340	345	350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn	355	360	365
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro	370	375	380
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe	385	390	395
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val	405	410	415
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly	420	425	430
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly	435	440	445
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly	450	455	460
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn	465	470	475
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly	485	490	495
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn	500	505	510
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr	515	520	525
Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly	530	535	540
Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu	545	550	555
Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly	565	570	575
Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn	580	585	590
Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr	595	600	605

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Gln Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Gln Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Gln Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:206:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCTCTGGTT GCGCGGGCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:207:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCGTGA GGCTCGAAAC CACCGACGG T

31

(2) INFORMATION FOR SEQ ID NO:208:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTGTGAATTC AGCCTTGGAA ATCTCTGGGA T

32

(2) INFORMATION FOR SEQ ID NO:209:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTCGCA

34

(2) INFORMATION FOR SEQ ID NO:211:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCGATCGGA GCGACGTGCC CACAACGGCC

35

(2) INFORMATION FOR SEQ ID NO:212:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAAGTCC GCTGCGG

36

(2) INFORMATION FOR SEQ ID NO:213:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7675 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGCGGAATGG GACGCGCCCT GTAGCGCGCG ATTAAGCGCG GCGGCTGTGG TGGTTACGCG	60
CAGCGTGACG GCTACACTTG CCAGCGCCCT ASCGCGCGCT CCTTCGCTT TCTTCGCCCT	120
CTTTCGCGCT ACGTTGCGCG GCTTTCGCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCGGATTG AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATGCGCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATACT GGACTCTTGT TCCAAACTGG AACACACTC AACCTATCT CGGTCTATTG	360
TTTGTATTG TAAGGGAATT TCGCGATTTC GGCCTATTGG TTAAGAAATG AGCTGATTGA	420
ACAAAAATTT AACCGGAATT TTAACAAAAT ATTAACGTTT ACAATTTCAG GTGGCACTTT	480
TGCGGGAAT GTGCGCGCAA CCGCTATTTC TTATTTTTC TAAATACATT CAAATATGTA	540
TGCGCTCATG AATTAATTCT TAGAAAAACT CATCGAGCAT CAAATGAAAC TCGAATTTAT	600
TGATATCAGG ATTATCAATA CCATATTTT GAAAAAGCGG TTTCTGTAAT GAAGGAGAAA	660
ACTGCGCGAG GCAGTTCCAT AGGATGGCAA GATCGTGTA TCGGTCTGGG ATTCCGACTC	720
GTCCCAATC AATACAACCT ATTAATTTC CCTCGTCAA AATAAGGTTA TCAAGTGAGA	780
AATGACATG AGTGACGACT GAATCGGTC AGAATGGCAA AAGTTTATGC ATTCTTTTC	840
AGACTTGTG AACAGCGCAG CCATTACGCT CCGCATCAA ATCACTCGCA TCAACCAAC	900
CGTTATTCT TGTGTATTGC GCGTGAGCGA GACGAAATAC GCGATCGCTG TTAAGAGGAC	960
AATTACAAC AGGAATCGAA TCAACCGCG CCAGGAACAC TCGCAGCGCA TCAACATAT	1020
TTCCACCTG ATCAGGATAT TCTTCTAATA CCGGAATGC TGTTTTCGGG GCGATCGCAG	1080
TGCTGAGTAA CCGATCATCA TCAAGGATAC CGATRAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATCCCT CAGCCAGTTT AGTCGACCA TCTCATCTGT AACATCATG GCAACGCTAC	1200
CTTTGCCATG TTTGAGAAAC AACTGCGCG CATCGGGCTT CCGATACAAT CGATAGATTG	1260
TGCGACCTGA TTCCCGGACA TTATCGCGAG CCGATTTATA CCGATATAAA TCAAGCATCA	1320
TGTTGGAAAT TAATCGCGCG CTAGAGCAAG ACGTTTCGGG TTGAAGATG CTCATAACAC	1380
CCCTGTGATT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCAAGACCAA AATCCCTTAA	1440
CGTGAGTTTT CTTTCCACTG AGCGTCAGAC CCGGTAGAAA AGATCAAAAG ATCTCTTTGA	1500

GATCCTTTT TTCTGCGGT AATCTGCTGC TTGCAACAA AAAAACCACC GCTACGAGG	1860
GTGGTTTGT TTCCGGATCA AGAGCTACCA ACTCTTTTC CGAAGGTAAC TGGCTTCAGC	1870
AGAGCGCAGA TACCAATAC TTCTCTCTA GTGTAGCGGT AGTTAGGCCA CCACTTCAG	1880
AACCTGTAG CACGCGCTAC ATACCTCGT CTCTAATCC TGTACAGT GGTCTGCTCC	1740
AGTGGGATA AGTCGTGTCT TACCGGTTG GACTCAAGAC GATAGTACC GGATAAGCG	1890
CAGCGGTGCG GCTGAACGGG GGGTCTCTGC ACACAGCCCA CCTTGGAGCG AACGACCTAC	1860
ACCGAATGA GATACCTACA GCTGAGCTA TGAGAAAGCG CCACTCTTC CGAAGGAGA	1920
AAGGGGACA GGTATCGGT AAGCGGCGG GTGGGAACAG GAGAGCGCAC GAGGAGCTT	1980
CCAGGGGAA ACCTCTGTA TCTTATAGT CCTGTCGGT TTGGCCACT CTGACTTGAG	2040
CTCGATTTT TGTGATGCTC GTGAGGGGG CGAGGCTAT GGAAAAAGC CAGCAAGCG	2100
GCCTTTTAC GGTCTCTGG CTTTTCTGG CCTTTGCTC ACACTGCTT TCTGCTTAA	2160
TCCCTGATT CTGTGATAA CCGTATTACC GCTTTGAGT GAGCTGATC CCGTCCCGC	2220
AGCGAAGCA CGAGGCGAG CGAGTCACT AGCGAGGAG CGAGAGAGCG CCGTAGCGG	2280
TATTTCTCC TTACGATCT GTGCGTATT TCACACCGCA TATATGGTG ACTCTCAGTA	2340
CAATCTGTC TGATGCGCA TGTTAAGCC AGTATACCT CCGTATCGC TACGTGACTG	2400
GGTCATGGT GCGCGCGAC ACCCGCAAC ACCCGCTGAC GCGCTCTGAC GCGCTTGTCT	2460
GCTCCCGCA TCGCTTACA GACAGCTCT GACCTCTCC GGGAGCTGCA TGTGTAGAG	2520
GTTCCTACC TCATCACCGA AAGCGCGAG CGAGCTCGG TAAAGCTCAT CAGCTTGCTC	2580
GTGAAGCAT TCAGAGATG CTGCTCTTC ATCGCGCTCC AGCTCTTGA GTTCTCGAG	2640
AAGCTTAAT GTCTGCTTC TGATAAAGCG GCGCATGTTA AGGCGGTTT TTCTCTGTT	2700
GCTACTGAT GCTCTGCTT AAGGGGATG TCTGTTCAAG GGGTAATGA TACCGATGA	2760
ACGAGAGAG ATGCTCAGCA TACGGTTAC TGATGATGA CATGCCGCT TACTGGAACG	2820
TTGTAGGCT AAACAACCTG CGGTATGGAT CGCGCGGAC CAGAGAAAA TCACCTCAGG	2880
TCAATCGCG CGTTCTGTTA ATACAGATG AGGTGTTCA CAGGGTAGCC AGCAGCTCC	2940
TGCGATGAG ATCGGAACA TAATGTTCA GGGCGCTGAC TTCCGCTTT CCAGACTTTA	3000
CGAAACACCG AAACCGAAGA CCATTCATG TTTTCTCAG GTGCGAGAG TTTTGCAGCA	3060
GCAGTCTCT CAGTTCTCT CCGGTATCG TGATTCATC TGCTAACAG TAAGGCAACC	3120
CTCGAGGCT AGCGGGTTC TCAAGGACAG GAGCAGGAT ATGCGCACCC GTGGGGCGC	3180

CATGCCGGCG	ATAATGCCCT	GCTTCGSCC	GAACGTTTG	GTGGCGGAC	CAGTACGAA	3240
GGCTTGAGCG	AGGGCCTGCA	AGATTCCGAA	TACCGCAAGC	GACAGCGCGA	TCATGCTCC	3300
GCTCCAGCGA	AAGCGGTCTT	CGCCGAAAT	GACCCAGAGC	GCTCCCGGCA	CCTGCTTAC	3360
GAOTTCGATG	ATAAGAAGA	CATCATAAG	TGCGCGAGC	ATAGTCATGC	CCCGCGCCCA	3420
CCGGAAGGAG	CTGACTGCGT	TGAAGGCTCT	CAGGGGCATC	GCTCGAGATC	CCGCTGCTTA	3480
ATGAGTGAGC	TAACTTACAT	TAATTGCGTT	GGCTCAGTG	CCCGCTTTC	AGTCGGGAAA	3540
GCTGCTGTC	CAGCTGCATT	AATGAATCGG	CGACGCGCG	GGGAGAGCGG	GTTTGCSTAT	3600
TGGCGGCGAG	GCTGCTTTT	CTTTTCACCA	GTGAGACGGG	CAACAGCTGA	TTCGCTTCA	3660
CGGCTGCGC	CTGAGAGAGT	TGCAGCAGC	GCTCCAGCT	GTTTTCGCG	AGCAGGCGAA	3720
AATCTGTGT	GATGCTGTT	AACGGCGGGA	TATAACATGA	GCTGCTTTC	GTATGCTGCT	3780
ATCCCATCTAC	CGAGATATCC	GCACCAACGC	GCAGCGCGGA	CTCGGTATG	GCGCGCATTC	3840
CGCGCGAGCG	CATCTGATCG	TTCGCAACCA	GCATCGCACT	GGGAACGATG	CGCTCATTC	3900
GCATTGCAAT	GCTTTCTTGA	AAACCGGACA	TGGCACTTCA	GTCGCTTTC	CGTTCCGCTA	3960
TGCGCTGAAT	TTGATTGCGA	GTGAGATATT	TATCCAGCC	AGCCAGAGCG	AGACGCGCGG	4020
AGACAGAACT	TAATGGCGCT	GCTAACAGCG	CGATTGCTG	GTGACCGAAT	GGGACCGAT	4080
GCTCCAGCGC	CAGTCCGCTA	CGCTCTTCAT	GGGAGAAAT	AATAGCTTTC	ATGGGTGCTT	4140
GGTCAGAGAC	ATCAGAGAAAT	AACGCGCGAA	CATTAGTGCA	GGCAGCTTTC	ACAGCAATGG	4200
CACTCTGGTC	ATCCAGCGGA	TAGTTAATGA	TGAGCGCACT	GACGCTTTC	GCGAGAAGAT	4260
TGTGACCGCG	CGCTTTACAG	GCTTCGAGCG	CGCTTCTTC	TACCATCGAC	ACGACCGAGC	4320
TGGCAGCGAG	TGATCGCGG	CGAGATTAA	TGCGCGGAC	CAATTGCGAC	GGCGCGTGCA	4380
GGGCGCACT	CGAGGTGCGA	ACCGCAATCA	GCACGACTG	TTCGCGCGC	AGTTGCTGTC	4440
CGACGCGGT	GGGAATGTAA	TTCAGCTCG	CGATCGCGC	TTCGCTTTT	TCCCGCTTT	4500
TGCGAGAAAC	GTGGCTGGCC	TGCTTCGCA	CGCGGAAAC	GGTCTGATAA	GAGACAGCGG	4560
CATCTCTGC	GACATCGTAT	AACCTTACTG	GTTCGACTT	CACGACCTG	AATTGACTTT	4620
CTTCGCGGCG	CTATCATGCG	ATACCGGAA	AGGTTTTCG	GCATTGATG	GTGTCGCGGA	4680
TCTGACGCT	GTCCCTTATG	CACTCTCTGC	ATTAGGAAGC	AGCCCACTAG	TAGCTTGAGG	4740
CGTTTGAGCA	CGCTCGCGCG	AAGGAATGCT	GCATGCAAGG	AGATGCGCG	CAACAGTCCC	4800

CGGCGCACGG GGGCTGGCAC CATACCCACG CGGAAACAG CGCTCATGAG CCGGAAGTGG	4860
CGAGCCCGAT CTTCGCCATC GGTGATGTGG GCGATATAGG CCGCAGCAAC CGCACCTGTG	4920
GGCGCGGTGA TGCGCGCCAC GATCGGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGGGA	4980
AATTAAATAG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCTT CTAGAAATAA	5040
TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCAGCTGAT	5100
CGACATCATC GGGACCAAGC GCACATCTCT GGAACAGGCG GCGGCGAGG CGGTCCAGCG	5160
GGCGCGGAT AGCGTCGATG ACATCCCGCT CGCTCGGCTC ATTGAGCAGG ACATGGCCCT	5220
GGACAGCGCC GGCAGAGTCA CCTACCGCAT CAAGCTCGAA GTGTGTTTCA AGATGAGGCC	5280
GGCGCAACCG AGGGGCTCGA AACTACCGAG CGGTTCGCTT GAAACCGGCG CCGGCGCCCG	5340
TACTGTGCGG ACTACCGCGG CTTGCTGCGC GGTGACGTTG GCGGAGACCG GTAGCAGGCT	5400
GCTCTAACCG CTCTTCAACC TGTGGGTTCC GGCCTTTTCA GAGAAGTATC CGAAGCTCAC	5460
GATCAAGGCT CAGGGGACCG GTTCTGTGTC CGGGATCGCG CAGGCGGCGG CCGGACGCT	5520
GAACATTGGG GCTTCCGAGC CTTATCTGTC GGAAGGTGAT ATGGCGGCGG ACAAGGGGCT	5580
GATGAACATC GCGGTAGCCA TCTCGGCTCA GCGAGTCAAC TACAACCTTC CCGAGTGAG	5640
CGAGCACCTC AAGCTGAACG GAAAAGTCTT GCGCGCCATG TACCAGGCGA CCATCAAAAC	5700
CTGGGACGAC CGCAGATCG CTGCGCTCAA GCGCGGCGTG AACTGCGCGG GCACGCGGCT	5760
AGTTGGGCTG CAGCGCTTGG ACGGCTCCGG TGACACCTTC TTGTTCAAGC AGTACCTGTC	5820
CAAGCAAGAT CCGGAGGCTT GGGGCAAGTC GCGCGGCTTC GGCACCAAGG TCGACTTCCC	5880
GGCGGTGGCG GGTGCGCTGG GTGAGAAGCG CAACGCGGCG ATGCTGACCG GTTGCGCCGA	5940
GACACGCGGC TGCGTGCGCT ATATCGGCAT CAGCTTCTTC GACCAAGGCA GTCAACGCGG	6000
ACTCGGCGAG GCGCAACTAG GCAATAGCTC TGCGAATTTC TTGTTGCGCG ACGCGCAAG	6060
CATTGAGGCG CGCGCGGCTG GCTTCGCATC GAAAACCGCG GCGAACCAGG CGATTTCGAT	6120
GATCGACGCG CGCGCGCGCG ACGGCTACCC GATCATCAAC TACGAGTAGC CCATGCTCAA	6180
CAACCGGCAA AAGGACGCGG CGACCGCGCA GACCTTGCGG GCATTTCTGC ACTGGGCGAT	6240
CACCGACGCG AACAAGGCGT GGTTCCTCGA CCAGGTTTCAT TTCCAGCGCG TGCGCGCGCG	6300
GTTGGTGAAG TTGCTGACG GGTGATCGCG GACGATTTCG AGCGCTGAGA TGAAGACCGA	6360
TGCGGCTACC CTGCGCGCAG AGGCAAGTAA TTTCGAGCGG ATCTCGGCGG ACCTGAAAAC	6420
CGAGATCGAC CAGGTGGAGT CGACGCGCAG TTGCTTCGAG GGCAGTGGC GCGGCGCGCG	6480

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GGGGACGGCC GCGGAGGCGG CGGTGGTSGG GTTCCAAGAA GCAGCCCAATA AGCGAAGCA 6540
GGAACTCGAC GAGATCTGGA CGAATATTCC TCGAGCGCGG STCCAATACT CGAGGCGGCA 6600
CGAGGAGCAG CAGCAGGCGC TGTCTCTGCA AATGGGCTTT GTGCCCACAA CGGCCGCTC 6660
CGCGCGCTCG ACCCTGCGAG CGCCACCGCG ACCGCGGACA CTTCTTGCCC CCGCACCACC 6720
GGCGCGCGCC AACACGCGCA ATGCCGAGCC GGGCGATCCC AACCGGACAC CTCGCGCGGC 6780
CGACCGGAAC GCACCGCGCC CACCTGTCTAT TCGCCCAAAC GCACCGCAAC CTCTCGCGAT 6840
CGACAACCGG GTTGAGGAT TCGCTCTGCG GCTGCTTCTT GCTTGGGTGG AGCTGAGCG 6900
CGCCCACTTC GACTACGCTT CAGCACTCTT CAGCAAAACC ACCGGGAGCC GCGCATTTCC 6960
CGGACACCGG CGCGCGCTCG CCAATGACAC CGTATCTGCG CTCGCGCGCG TAGACCAAAA 7020
GCTTTACGCT AGCGCGGAAG GCACCGACTC CAGGCGCGCG GCGCGGTTGG GCTCGGACAT 7080
GGGTGAGTTC TATATGCGT ACCCGGGCAC CGCGATCAAC CAGGAAACCG TCTGCTTGA 7140
CGCGAACCGG GTTCTGGGAA GCGCTCTGTA TTACGAAATC AAGTTACGCG ATCGGAGTAA 7200
GCGGAACCGC CAGATCTGGA CGGCGCTAAT CGGCTCGCCC GCGGCGGAAG CACCGGAGCC 7260
CGGCGCGCGT CAGCGCTGCT TTGTGCTAIG GCTCGGGACC GCGAACAAAC CGGTGACAA 7320
GGGCGCGCGC AAGCGCTCG CGAATCGAT CGGCGCTTGG GTGCGCCCGC CGCGCGCGCC 7380
GGCACCGCGT CCGCGAGAGC CGGCTCGGCG GCGCGCGCGC GCGGGGGAAG TCGCTCTAC 7440
CGCGAGCACA CGACACCGC AGCGGACCTT ACCGCGCTGA GAATTCTGCA GATATGATC 7500
ACACTGCGCG CGCTCGAGC ACCACCAACA CCACCTGGA GATCGCGCTG CTAACRAAGC 7560
CGGAAGGAA GCTGAGTGG CTGCTGCGAC CGCTGAGCAA TAACTAGCAT AACCGCTGG 7620
GGCGCTTAAA CGGCTCTTGA GCGCTTTTTT GCTGAAGGA GGAATATAT CCGGAT 7676

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(X) INFORMATION FOR SEQ ID NO:214:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:214:

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Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1             5             10             15
Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

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20 25 30
 Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35 40 45
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50 55 60
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65 70 75 80
 Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85 90 95
 Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
 100 105 110
 Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
 115 120 125
 Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
 130 135 140
 Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
 145 150 155 160
 Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
 165 170 175
 Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
 180 185 190
 Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Glu Gly Thr Ile
 195 200 205
 Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
 210 215 220
 Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
 225 230 235 240
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
 245 250 255
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
 260 265 270
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
 275 280 285
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
 290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320

Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Gln Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(12) INFORMATION FOR SEQ ID NO:215:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GTGGCGGGCG	TCGGCGGGCG	CAGCAGAGCG	ATGTGCATCC	GTTCGCGAAC	CTGATCGCGG	60
TCGACATGCA	GCCTGCGGAA	CGCTGCGGAG	ACGAGAGACG	TCAGGAGCGC	GTCCAGCAGC	120
GGGTTCCGCG	CGGTGACGAA	GGTACCGCG	TGCAGATCA	GCAGCACCCG	GGCGATGGCG	180
CGGACCAATG	TCGACCGGCT	GATCGCGCGC	ACGATCCGCA	CCACCAAGCG	CACGAGGAGC	240
ACACCCAGCA	GGCGCGCGCT	GAACCGCCAG	CGCAATCGCT	TGTGACCGAA	GATGCGCGTC	300

CCGATCGCGA	TCAGCTGCTT	ACCCACCGGC	GGTGAACCA	CCAGGCCGTA	CCCGGGTGTG	340
TCCTCCACCC	CATGGTGTG	CAGCACTGC	CAGGCTTGGC	GGTGCSTAA	GCTTCGTGTC	420
GAAGATGGGG	GTCCCGGCAT	CGTACCGA	GCCC			454

(2) INFORMATION FOR SEQ ID NO:216:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGCAGAAGTA	CGCCGATCC	TCGGTGGCCG	ACGCCGAACG	GATTGCGCCG	GTGCGCGAAC	60
GCATCTCTCC	CACCAAGAAAG	CAAGGCAATG	ACGTCTGTCT	CGTCTGTCT	GCCATGGGGG	120
ATACCAACCGA	CGACCTGCTG	GATCTGGCTG	AGCAGGTGTG	CCCGGCGCCG	CGGCTCGGG	180
AGCTTGACAT	GCTGCTTACC	CCCGGTGAAC	GCATCTCGAA	TGGCTTGGTG	GCCATGCCCA	240
TGGAGTCCCT	CGCCCGCGAT	GCCCGTCTGT	TCACCGGTTT	GCAGGCGCGG	GTGATCACCA	300
CCGGCACCCA	CGGCAACGCC	AAGATCATCG	ACGTCAAGCT	GGGGCGCGTG	CAAAACCCCC	360
TTGAGGAAGG	GGGGTCTGTC	TTGGTGGCCG	GATTCGAAGG	GGTCAGCCAG	GACACCAAGG	420
ATGTCACGAC	GTTGGGCGCG	GGCGGCTCGG	ACACCAACCG	GGTCGCCATG		470

(2) INFORMATION FOR SEQ ID NO:217:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGCCGCGGTA	CCCGGCGCGG	ACAAACAACG	ATCGATTGAT	ATCGATGAGA	GACGAGGAA	60
TGGTGGGCTT	TCCCGAGTTG	ACCGACGAGC	AGCGCGCGCG	CGCGTTGGAG	AAGGCTGGTG	120
CCGCACTGCG	AGCGCGAGCA	GAGCTCAAGG	ATCGGCTCAA	CGGTGGCGGC	ACCAACTTCA	180
CCGAGTCTCT	CAAGGACGCG	GAGAGCGATG	AAGTCTTGGG	CRAAATTAAG	GTGTCTGGCG	240
TGCTTGAGGC	CTTGCCCAAG	GTGGCAAGG	TCCAGGCGC			279

(2) INFORMATION FOR SEQ ID NO:218:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACACGGTGG	ACTCGACGAG	CCCTCTGTTG	AGGTGTGAC	CGACAAGGTC	GACACCGAAA	60
TCCTCTGCGG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGCTGGA	120
GGTGGCGGGC	GAGCTCTCTG	TCATTGCGGA	CGCCCATSAT	GCCGGCGAGG	CCGCGGTCCC	180
GGCACCOCAG	AAATCTCTG	CCGCCCCAAC	CGAATCGA			219

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCCTGCGGA	CATCGGCGCC	GCCCGCGCC	CGAAGCCCGC	ACCAAGCCG	GTCCCGGAGC	60
CAGCGATGCG	GCCGAAGGCC	GAACCCGCGC	CATCGCCGCG	GGCGGCCGAG	CCAGCCGGTG	120
CGCGCGAGGG	CGACCGCTAC	GTGACGCGCG	TGGTGCAGAA	GCTGGCGTCC	GAAGAACACA	180
TGACCTCGC	CGGGGTGACC	GACCCCGGAG	TGGTGTGTCG	CATCCGCAAA	CAGGATGTGC	240
TGGCGCGCGC	TGAACAAAG	AAGCGGGCGA	AAGCACCGGC	GCCGCGCGCC	CAGGCGCGCG	300
CGCGCGCGCG	CGCAAGCG	CCCTCTGAG	ATCGATGCC	GC		342

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGGT	CAGTATCAGC	GCGACGAGG	ACGCCACCGT	GCCCTCGCGC	GGCGAGTTGG	60
CCCGGATCGG	TGTCGCTGCG	GACATCGCGG	CGCGCGCGCG	CCCAAGCCG	GCACCCGAGC	120
CGTCTCCCGA	GCGAGCGCGG	ACGCCGAAGG	CGGAACCCGC	ACCATCGCGG	CCGCGCGCGC	180
AGCGAGCGCG	TGCGCGCGAG	GCGCGACCGT	ACGTGACCGC	GCTGGTGCGA	AGCTGGCGCT	240
CGGAAACAAA	CATCGACCTC	GCGGGGTGA	CGCGACCGCG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGCGCGCG	GCTGAACAAA	AGAAGCGCGG	GAAGACACCG	CGGCGCTGAG	360
CGCTTCATCA	CCCGGTTAAC	CAGCTTGCCG	CGAAGCGCGG	CTTCGACCTC	TTGCGGGGTC	420
TTGCTCCGCT	CGAGCGCGTC	GCGGAGCCAG	TTGAGTTAG	GCGCGCGAAA	TCCTCCAGTT	480
CGCCAGGAAG	GCGACCCGGA	ACAGGCTCGG	CACCC			515

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CGGACCCCAA	GGTCGAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACCC	CACCAAGCCG	60
TGACTCAACA	GGCGGCGCAA	GTGATCGGTA	ACCAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGGC	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAGAGCCCTG	ACGCTGGCCG	180
ACCAGGCCAC	GGCGGCGGGA	GACGCTGCCA	AGGCCACCGA	ATACAACAAC	GGCGGCGAGG	240
CGTTCCGACG	CGAGCTGGTG	ACCGKCGAGC	AGAGCGTCTG	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCGGT	CGAACGAAAT	GGATGTGTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACCCAGC	TGCTCAGCCA	GCTCGAGCAG	GGAGAGATGC	420
AGSAGCAAGT	CAGCGCATCG	TTGCGGTGCA	TGAGTGAGCT	CGCGGCGCCA	GGCAACACGC	480
CGAGCTGCGA	CGAGGTGCGC	GACAAGATCG	ACCGTGCCTA	CGCAACCGCG	ATCGGTTCCG	540
CTGAACCTGC	CGAGAGT					587

(2) INFORMATION FOR SEQ ID NO:222:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTGACATCC	ACCTGGGTTT	GGCAGCGGT	GGCGAGCGT	GTGATAGCC	60
AGAGGTGGAC	CTGCGCCGAC	CGACGATCGA	TGAGGAGTCC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTGGGT	GAGAGCGTCA	CGAGGGGAGC	GGTTACCGGC	TGGCTCAAC	180
AGGAAGCGGA	CACGGTGGAA	CTCGACGAGC	CCCTCGTGGG	GGT		223

(2) INFORMATION FOR SEQ ID NO:223:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAGTACA	TGTCGCGGTC	GATGTGCGCG	AACCCGCGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CGGCATAACG	CCAGTCCCGG	CGCAGAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CGCGGAGCCA	CCACATCGCG	GGCGTGCCHA	CGAGCATCTC	GGCCTTGAGC	180
CACGACTGTG	CGCCGACGCT	TGCACTCTCT	TGCTGGTCTG	TGGGCTACAG	CACCGGCGCG	240
AACGACATGG	CGCAGGTCCA	CGGTTTGGAT	TCCCAAGGCT	GGTAGTTGCC	TGCGGAATTC	300
GTGAGGCGCG	CGTGGAAGTG	GAACGCTTTG	GGCGTGTATT	GCCAGAGCGA	GGCGACGGCG	360
TGGGGCAGCG	GAACAACCGA	GTTGCGAGCG	ACCGTTTGAC	CGACCGCATG	CGGATCGCAT	420
GGGCTCTCGG	ACCGCAACCA	CGGAGCGTAG	GTGCGCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCGAGCGCAT	ACCGGCTGGG	AAGCACGCTCA	CGCTCGCACTG	TTCCCGACCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTCGCGC	CGCCAGCTCA	ACCGCAGC			578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCGACG	CGCGGCGCGG	TTGAGACAAG	CTGCTGCCGC	ACGTGAGCGG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GGTCTCTAAG	GACGCGGAGA	180
GCATGAAAT	CTTGGGCAAA	ATGAAGGTGT	CTGGCTGCT	TSAGGCGCTTG	CCAAAGGTGG	240
GCAGGCTCA	GGCGCAGGAG	ATCATGACCC	AGCTGGAAAT	TGCGCCCGAC	CGCGCGGCT	300
TGTTGGCGTC	GGTGACCGTC	AGCGCAGGCG	CTGTCTGAA	AAGTTCGGCT	CGCGCTAACG	360
CGCGCGCGCG	ACGATGCGCG	CGCGAAGCGC	TGTGTGGCG	GTACCGCGCG	ATACGGGGGA	420
GAAGCGGCTT	GACAGGGCCA	GCTCACAATT	GAGGCGGAAC	GGCCCGGTGG	GGGGGAACCC	480
GGCC						484

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGGACTGCGA	CGCGGACCGA	CCACATCGCG	GGCTGCGCGA	CCAGCATCTC	GGCTTTGAGG	60
CACGACTGTG	CGCGCGAGCG	TGCACGCTCT	TGCTGGTCSA	TGGCGTACAG	CACCGGCGCG	120
AACGACATCG	GCCAGGTCCA	CGGTTTGAT	TCCCAAGGGT	GGTAGTTGCG	TGCGGAATTC	180
GTGAGGCGCG	CGTGGAAAGT	GAACGCTTTG	CGGTTGTAGT	GCCAGAGCGA	GCGCACCGCG	240
TGCGGCACCG	GAACACCGGA	GTTCGCGACG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
CGGCTCTCGG	ACCGCAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	360
CCGAGCGCAT	ACCGCTGAGG	AAGCACCTCA	CGCGGCACTG	TCCCGAGCGA	CGGTCTTTGC	420
ACTTGCTACT	GAGTCTCGCG	GCCACGCTCG	AACGCGAGCG	CGATCGCGCG	GAGGACACGC	480
ACGAAGTACA	CGCGGACCGA	CTTGTGTGGG	CAAGCCCAATC	CCAGCAGACA	CCCCGCGC	537

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1           5           10           15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
 20           25           30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
 35           40           45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
 50           55           60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
 65           70           75           80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
 85           90
  
```

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1           5           10           15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
 20           25           30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
 35           40           45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
 50           55           60
Val Ser Ala Gly Pro Thr Arg Ile
 65           70
  
```

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1 5 10 15
 Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
 20 25 30
 Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
 35 40 45
 Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50 55 60
 Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
 65 70 75 80
 Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
 85 90 95
 Gln Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
 100 105 110
 Pro

(12) INFORMATION FOR SEQ ID NO:231:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1 5 10 15
 Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
 20 25 30
 Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
 35 40 45
 Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Glu Pro Ala Gly Ala
 50 55 60
 Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
 65 70 75 80
 Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
 85 90 95
 Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Glu Gln Lys Lys Arg
 100 105 110
 Ala Lys Ala Pro Ala Pro
 115

(12) INFORMATION FOR SEQ ID NO:232:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
 20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
 35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
 50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
 65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
 85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Ala Gln Ala Lys Lys Ala
100           105           110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
115           120           125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
130           135           140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145           150           155           160
Ser Leu Asp Gln Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
165           170           175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
180           185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
 20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
 35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
 50           55           60
Leu Asp Glu Pro Leu Val Glu
 65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1      5      10
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
 20      25      30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
 35      40      45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
 50      55      60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
 65      70      75
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
 85      90      95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
100     105     110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
115     120     125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
130     135     140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
145     150     155
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
165     170     175
Arg Ser Leu His Leu Val
180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Ile Val Ala Leu Pro
 1      5      10
Gln Leu Thr Asp Glu Gln Arg Ala Ala Ala Leu Glu Lys Ala Ala Ala
 20      25      30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
 35      40      45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
 50      55      60

```

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid